

(1 of 90)

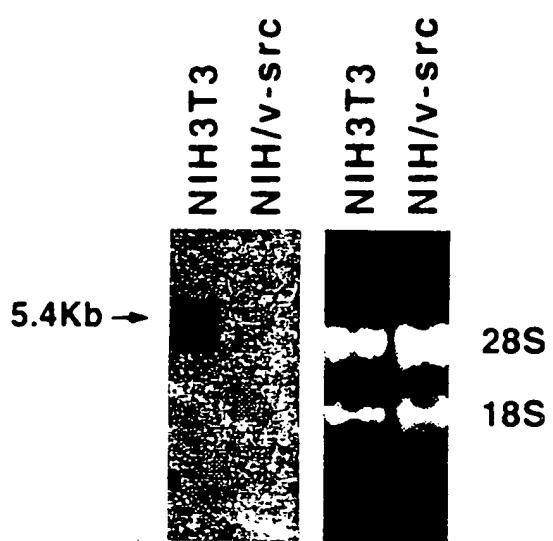


FIG. 1

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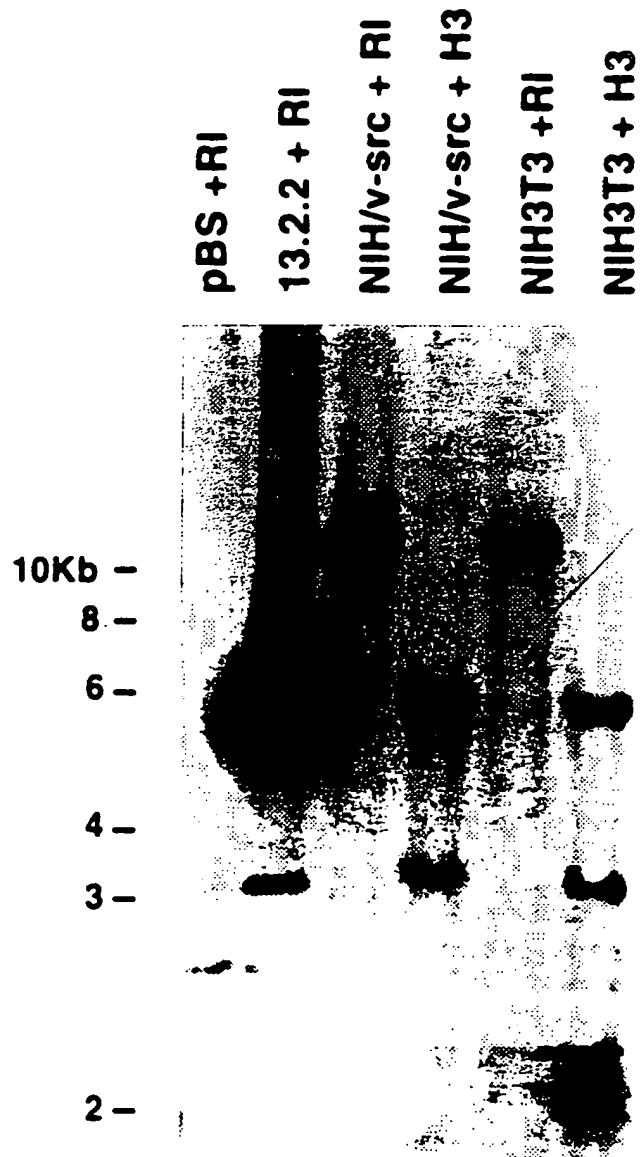


FIG.2A

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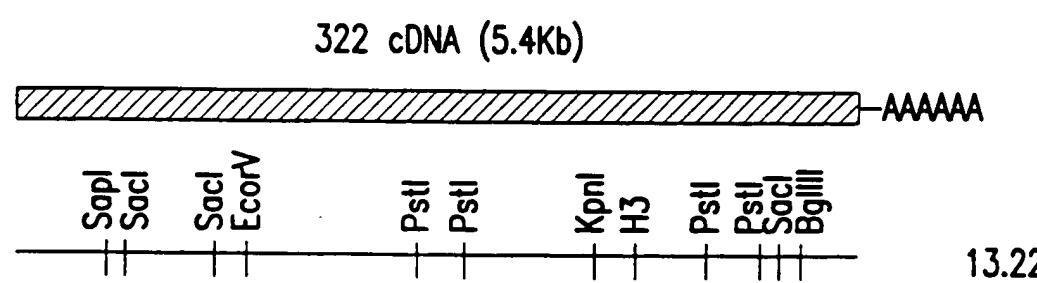


FIG.2B

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	ggaaaagacagccaggcctcgaggaggcaggagccggagaaggacacagaccaggccag	60
	gttgtcaggcactacagaagggtggagctgcccatttggaaaccaggltgtgacctgg	120
	gycatcgtagggagaatgtgtgtccctttggcaacggaaagtgtttgtgagaatggg	180
	M E	2
181 3	agccccaccaaaaagt!gttgcaagggtccacgtggacccgtggagaagacagaggaggaa	240
	A H Q F V A E V S T V E K T E E E	22
241 23	qcaggaggaggaggaggctgaaagggggggtgggtggtagaaggaaacaggaaatccct	300
	Q <u>G</u> <u>G</u> E A E G Q V V V E G 1 G F S L	42
301 43	gccccctgaaaaactgtggctgaggcccaggagggtcccccaggaaaggctggcgtggagga	360
	P P E K I A E p Q F V P Q E A E P A E E	62
361 63	gctgtggaaaggcagagagatgtglgtctctggaggagaccacactcaactgacagacct	420
	L M K S R E M C V E G G D H T Q L T D L	82
421 83	aagtccctgaaaggagacgtgcctccaaacacccaggaaaggcattgtcaagtggaggat	480
	S P E E K T L P K H P E G I V S E V E M	102
481 103	gctgtcccttcaggaaaaaatcaaggtaacaggaaagtcccttgaagaaactcttcgttag	540
	L S S Q E R I K V Q G S P L K K L F S S	122
541 123	ctcaggcttaaaaaggctgtctggaaagaaggcagaaggggaaacgggggggtggggaga	600
	S G L K K L S G <u>K</u> <u>Q</u> <u>K</u> G K R <u>G</u> <u>G</u> D	142
601 143	cgaagagccctggagaataccaacacattcacaccgaatccccagaggtgtgatgagca	660
	E E P G E Y Q H I H T E S P E S A D E Q	162

FIG.3A

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661 163	gaaggaggagagctctcgccgtccccgaggaggaccacgtgtctggagaa K G E S A S P E E P E T T C L E K	720 182
721 183	agggccgtggaaaggccccaggatggggaaagctggaaactacttcgtggagaaa G P L E A P R M G K L R K E L L R G E [K]	780 202
781 203	gaagagggaggatcaactcccgtggcatccttcaaaaatggatggacacccaaacgt [K R K] D H S L G I L Q K D G D T Q E T V	840 222
841 223	cgcgaaggacccttctgagaqtgacaaggaggaaagactggagaaggtaaaggcgccacctt R R P S F S D K F E L Q K D T Q E T V	900 242
901 243	glccctccacatgtacatgtcagaataalgtcaaggatgaagtcaaggcgcc S S T D S T V S E M Q D E V K T V G E I L	960 262
961 263	acaaaaaggccaggaaaccaaaggcgtaagggtggatacttcagggtctttggaaagcaactgtat Q K P E P K R V D T S V S W E A L I	1020 282
1021 283	tgtgtcgatcatccaaaggaggaaaggcatccatcttcaggatataaaggggcc C V G S S K [K R A R] K A S S D I R G P	1080 302
1081 303	aggcacactggggggacagtacaggaggccaggaggccaggcaaaaaggcc R T L G G Q S O S R G Q Q R S R	1140 322
1141 323	aaacagacgtgttccgtccggccaggaggccaggaggccaggcaaaaaggcc T D A V P A S T Q E Q D Q A Q G S S S P	1200 342
1201 343	cggccaggggaaaggcccttcggaaagggtgtctccacttggggatcattaaaag E P A G S P S E G V S T W E S F K R	1260 362

FIG. 3B

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1261 363	attagtcaactccaagaaaaaatccaaagtcaaaaactggaaaggagaaaaaggccgaaaggac L V T P R [K K S K] S K L E E K E A G R T	1320 382
1321 383	tctagttgttagggagggttgtccacttagatcgAACCGTgttagagaatcttgggt L V V G A G C P L R S N R V E K N L G F	1380 402
1381 403	tccattaaagaat!catccccggacgggaagaaaaggccatggaaaggcaagaaca P L R N S S P D G G R K G Q M G R Q E Q	1440 422
1441 423	agccactgtggaaaggactcaggcccagtggagataaatggggacgaggcctgtatgtcccagc A T V E D S G P V E I N E D E P D V P A	1500 442
1501 443	agtcgtgcccttgtcttgtatgcgttgtggctgttagtgtccggaggctcagtaagaactctgt V V P L S E Y D A V E R E K M E A Q G N	1560 462
1561 463	tgcggaggctgcccaggctgtggctgttagtgtccggaggctcagtaagaactctgt A E L P S C W G C V V S E E L S K T L V	1620 482
1621 483	ccacactgtggaggctgtcgaggcattgtatggggaccaggcaggcgttccagggttcgaaggaggcg H T V S V A V I D G T R A K T S K E E R	1680 502
1681 503	gtctcccttgtggatatcccgcttccgtaaacagaacacacagcgggagaagc S P S W I S A S V T E P L E H T A G E A	1740 522
1741 523	cattggccacctgttgaaagggtcactgtggaaaaggacatcatgtcagaaggaaactccctgtgt M P P V E E V T E K D I I A E E T P V L	1800 542
1801 543	cacccagaggttaccagggttaaagatgccatgacgacatggtaaccaggtaatgg T Q T L P E G K D A H D M V T S E V D	1860 562

1861 563	tttacctcagaaggctgtacagccacagagaccctcaggaggcttcgtactgaagaagt F T S E A V T A T E T S E A L R T E E V	1920 582	
1921 583	taccaagcatcgggccgaaaggaccacagacatggtgcccaattccaggctgac T E A S G A E E T D M V S A V S Q L T	1980 602	
1981 603	tgactccccagacaccacagagaaggccaccaggttcaggaggtagagggtggtgtct D S P D T T E A T P V Q E V E G V L	2040 622	
2041 623	agatacayaqaqaqqaqcgcacacycaggccatcccaaggccgttgcaqacaaggat D I E F F R Q T Q A I I Q A V A D K V	2100 642	
2101 643	gaaaaggaggcccagggtccgtgtacccaggactgtcggagaacggggctcaaaaggact K E L S Q V P A T Q T V Q R T G S K A L	2160 662	
2161 663	gagaaagggttggaggtagaggaggactccggaaagtgtggcttcggagaaaggaaagg E K V E D S E V L A S E K E K D	2220 682	
2221 683	cgttatgccaaaggaccgtcgaggaaagtggactgacaggcatcttcacaggctctga V M P K G P V Q E A G A E H L A Q G S E	2280 702	
2281 703	gactggacaggctactccagaggcccttgaagtttcctgtggactcagcagatgtggacca T G Q A T P E S L E V P E V T A D V D H	2340 722	
2341 723	tgtcgccacgtggccaggtttatcaaggctccaggcactgtggaaacaggccgtggccctgt V A T C Q V I K L Q Q L M E Q A V A P E	2400 742	
2401 743	gtcatccgaaaccttgcacagacactgtggacaaatggaaaggcactccctttagcaggattcaga S S E T L T D S E T N G S T R L A D S D	2460 762	

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**FIG. 3D**

**FIG.3E**

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2461 763	cactgcagatggcacacaaggatgaaaccattgacaggacacttgcaggactaaaggccactgc T A D G T Q Q D E T I D S Q D S K A T A	2520 782
2521 783	agctgtcaggcagtcacaggtcacagaagaaggcggtactgtctcagaaaaaggaggagcc A V E Q S Q V T E E A A T A Q K E E P	2580 802
2581 803	ttcgacactacctaataatgttlccagccaggaaacaatggggaaaccaggaaaggaga S T L P N N V P A Q E E H G E E P G R D	2640 822
2641 823	tgtttttgaatctacacacgcaaggagcttgctgtcgaggcggtccccgtctggcaaaagac V L E P T Q Q E L A A A V P V W Q K T	2700 842
2701 843	ttaggttggtaaaggagggttgactgggtggatggatggaaaaagtcaaaggaaaca E V G Q E G L V D W L D G E K V E E Q	2760 862
2761 863	ggagggttgttgcacactctggaccccacagtcaaaaggctgtctgtacatgtacag E V F V H S G P N S Q K A A D V T Y D S	2820 882
2821 883	tgaagtgtatggaggtgtgggggttgcaggaaaaggaggtactgtcagggttttag E V M G V A G C Q E K E S T E V Q S L S	2880 902
2882 903	cctggaggaggatgaaactgtacgtttggaaaaggagacaaggccaga L E E G M E T D V E K E K R E T K P E	2940 922
2941 923	gcaagtgtatggatggcggatggcgttgcgtatggatggactacgg Q V S E E G E Q E T A A P E H E R N Y G	3000 942
3001 943	gaaggccaggcgttgcacacttgcacatgcccaggctcagagggggaaaggcactggggaaaggcc K P V L T L D M P S S E R G K A L G S L	3060 962

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3061 963	tggagaaaggcccttctccagaccaagacaagaacaaaggcaggttgcataaggltcaagttca G G S P S I P D Q D K A G C I E V Q V Q	3120 982
3121 983	aaggcctggacacaaacagtcaactaaaaacaggcagaaggctgtggaaaaggatcatagaaaacgg S L D T V T Q T A E A V E K V I E T V	3180 1002
3181 1003	tgtgatttcagagacagggtgaaaaggccaggatgtgttaggtgcacacattaccaggctga V I S E T G E S P E C V G A H L L P A E	3240 1002
3241 1023	→Zn-finger→ 9aagtcccttgcacgggtggccactggactctcaggatgcagaggacacgggtacccct K S S A T G G H W T L Q H A E D T V P L	3300 1042
3301 1043	ggggcctgaggctcaggcagaatccatccatcatgttaactccctgcctgaaaaggcac G P F S Q A F S I P I I V T P A P E S T	3360 1062
3361 1063	cctacatccctgacctaaggagaataaggcgcatcccacaaaggcgatcaggaaaga I H P D L Q G E I S A S Q R E R S E E	3420 1082
3421 1083	ggacaaggccagatgtggcctgtatgtgcacggcaaggaggatcagcaatcgacaaagt D K P D A G P D A D G K E S T A I D K V	3480 1102
3481 1103	cctcaaggctgaaaccttgagatcctggaaacttgagatgtggaaacaaggatgtgtgctgaa L K A E P E I L E L E S K S N K I V L N	3540 1122
3541 1123	cglcattcagacaggccgttgaccaggttcgcaacgtacagaaaaacagcccccaaactcatgc V I Q T A V D Q F A R T E I A P E T H A	3600 1142
3601 1143	ttatgattcacagaccagggttcctgcaatgcgcgttggacaggcaggccaaacagatg Y D S Q T Q V P A M R L D S R E P N R C	3660 1162

FIG.3F

TRANSCRIPTION

3661 1163	ctggacaaaaatgaaagtgc caaagat gaaacacccat gccccaggaggactt W T K M V A K M K H P V P R E D L	3720 1182
3721 1183	gcaaglcctgaccgttc tgaggcatggctca gctcg gaaatgc ttgc cgc tttgc agt Q V L T V L E A W L S S E M L A A L A V	3780 1202
3781 1203	t gaaaaggccggltcaaa agtaaggcattgagaagactgc ctca accccaa aqat caaa E S A G V K V S I E K L p p Q P K D Q K	3840 1222
3841 1223	ggagcatgcttgatggccctca gctcca a aagcttaaggccaggcaggc aqgtlgtclgg E H A D G P Q L Q S I A Q A E V S G	3900 1242
3901 1243	aaacctaacccaa a gaaatccc gagacacc a a ccc a a ccc a a a g c t a a c c N I I K F S P D I N G p K L T E E R C P	3960 1262
3961 1263	ccaaaaagg ttaggtccaggaa a a a a a t g t c a c t a a a g t c a g t c a a a g g a a Q K L R S R K K C L P S Q R T R P	4020 1282
4021 1283	caggcaggaaaggacc tgcaggaggccaaaggagac ctggcagaat ccta a a g t t a g t R Q K R T C R S Q R E T W Q N P K M L V	4080 1302
4081 1303	t gctcat t q t a c a t c t gta a g a c c a a g a a t g t g a a a a a c a a g t A H C T S V R P E C E N K S Q N K M L L	4140 1322
4141 1323	gttgggacc tttggacca a a g a t t c a g a g c c a t c a g a g a c a g g c c g t c c a a t L G P W T K I S E P M R S R E Q G R P M	4200 1342
4201 1343	gatttccacccaggtagaggcacccgacaatttctgaggctcatcggagactagaggcc a g c I S T Q *	4260 1346

(10 20 90)

FIG. 3G

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**FIG. 3H**

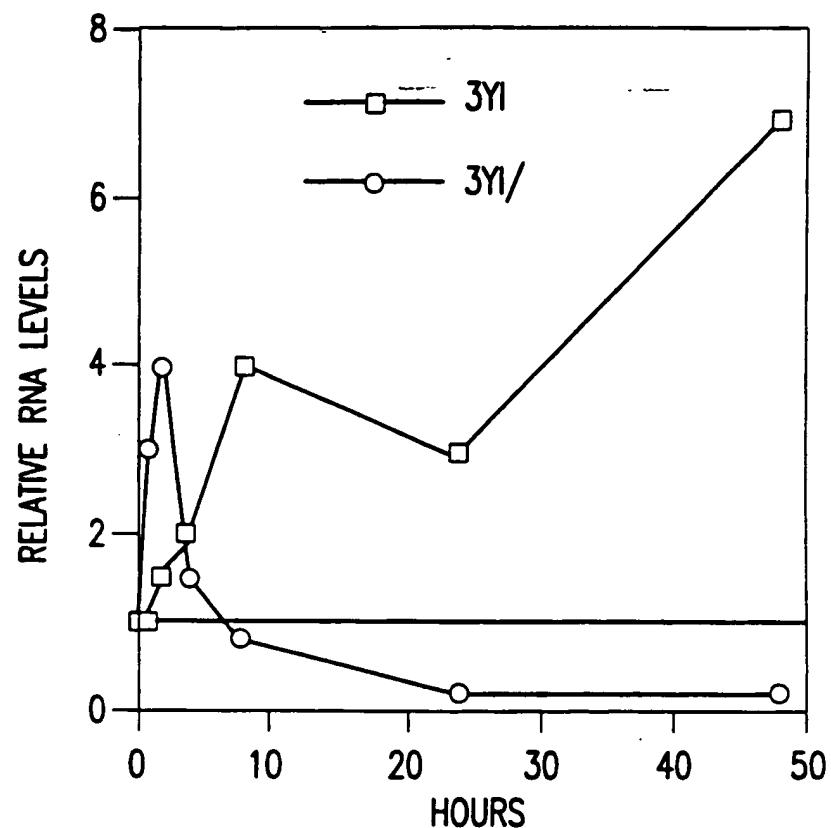


FIG.4A

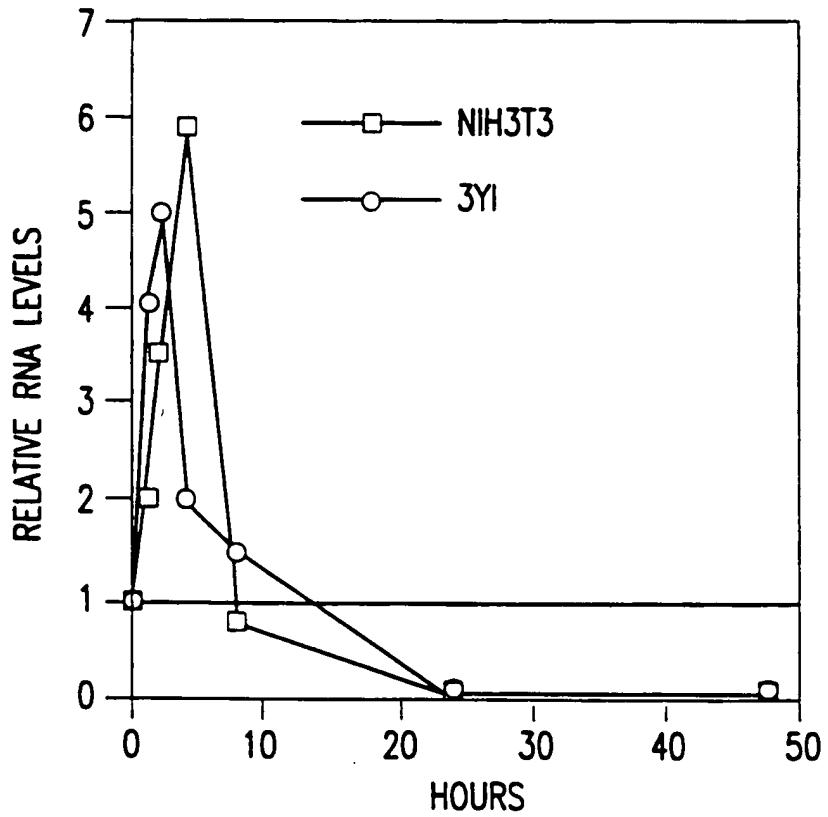


FIG.4B

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rat-6  
rat-6/rat-1  
rat-6/les  
rat-6/neu  
rat-6/myc  
rat-6/src  
rat-6/mos



FIG.5

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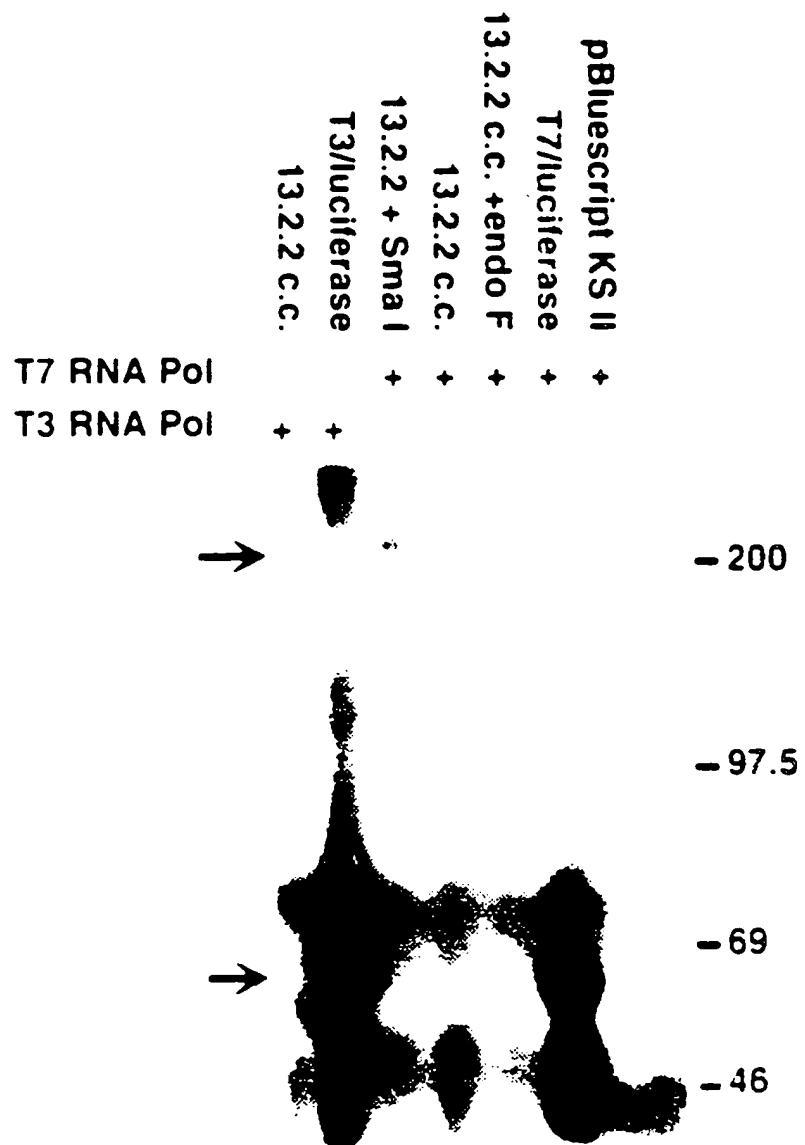


FIG.6

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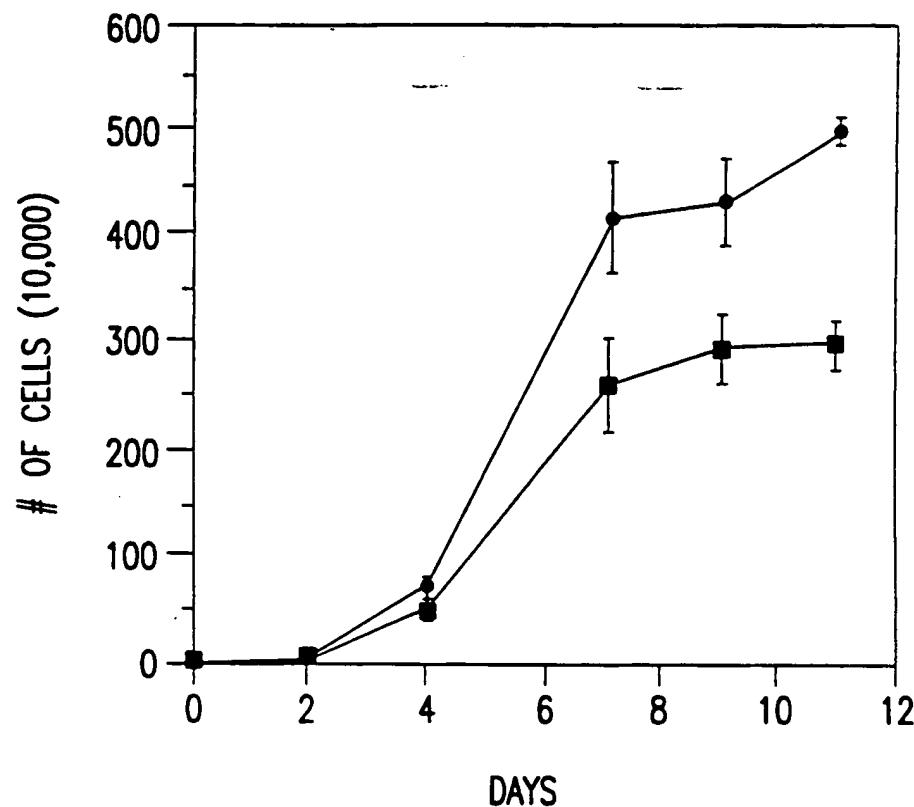


FIG.7A

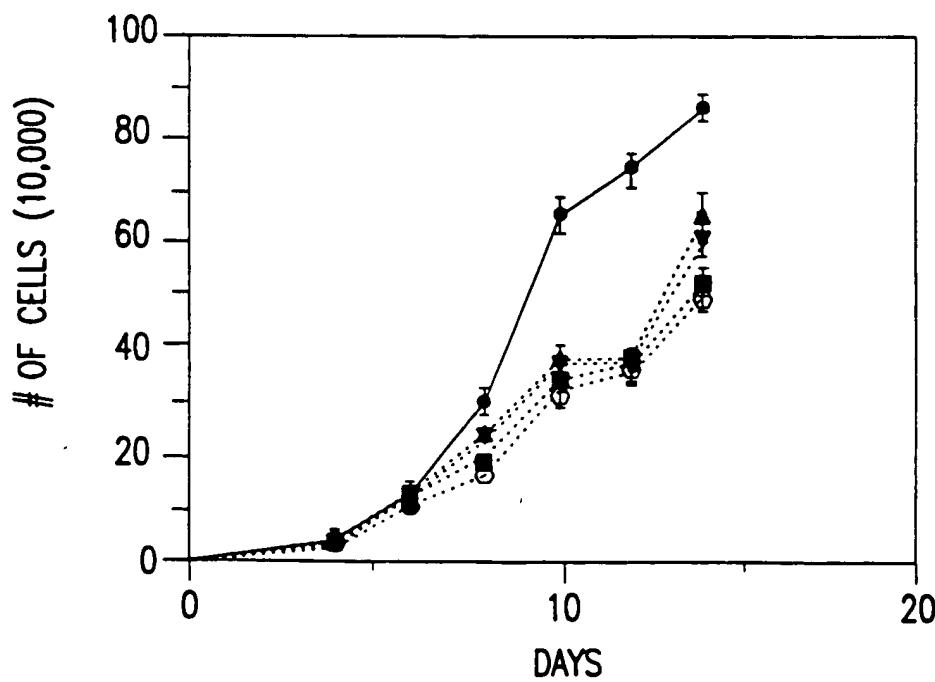


FIG.7B

F00740 - 22120666

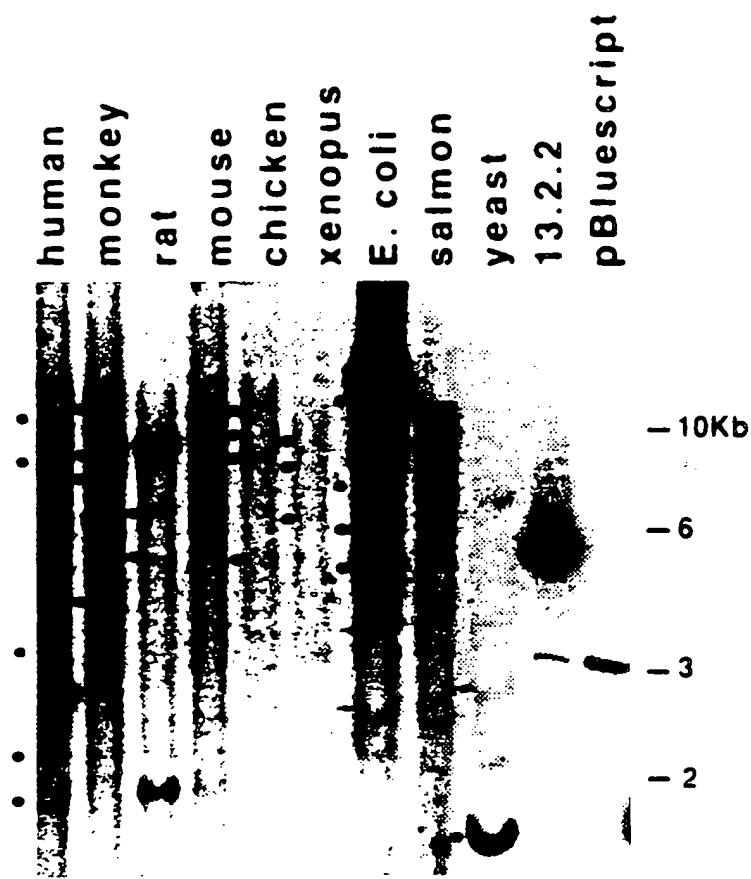


FIG.8

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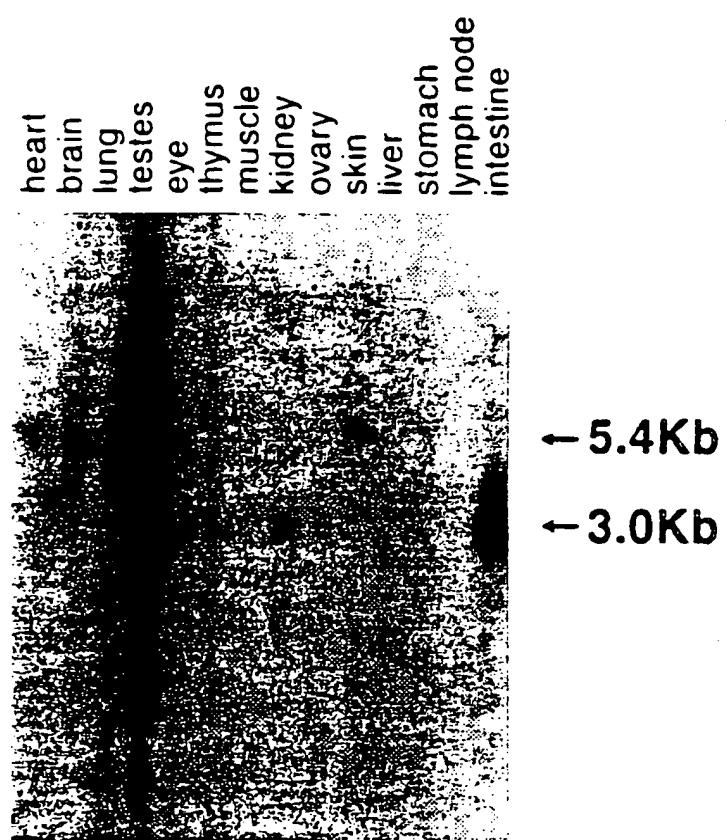


FIG.9

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9            18            27            36            45            54

5' ATG GGC GCA GGC AGT TCC ACC GAG CAG CGG AGC CCC GAG CAG CCG GCG GGG AGC  
-----  
M G A G S S T E Q R S P E Q P A G S

63            72            81            90            99            100

GAC ACG CCG AGC GAG CTG GTG CTC AGT GGC CAT GGG CCC GCA GCT GAA GCC TCG  
-----  
D T P S E L V L S G H G P A A E A S

117            126            135            144            153            162

GGA GCA GCT GGA GAC CCC GCC GAC GCG GAC CCC GCC ACC AAG CTC CCA CAG AAG  
-----  
G A A G D P A D A D P A T K L P Q K

171            180            189            198            207            216

AAT GGC CAG CTG TCT TCT GTC AAC GGC GTA GCT GAA CAA GGA GAT GTC CAT GTC  
-----  
N G Q L S S V N G V A E Q G D V H V

225            234            243            252            261            270

CAA GAG GAA AAC CAG GAG GGG CAG GAG GAA GAA GTC GTT GAT GAG GAT GTT GGA  
-----  
Q E E N Q E G Q E E E V V D E D V G

279            288            297            306            315            324

CAG CGA GAG TCA GAA GAT GTG AGA GAA AAA GAC CGA GTT GAA GAA ATG GCG GCC  
-----  
Q R E S E D V R E K D R V E E M A A

333            342            351            360            369            378

AAC TCC ACA GCT GTT GAA GAT ATC ACA AAG GAT GGG CAG GAG GAG ACA TCA GAA  
-----  
N S T A V E D I T K D G Q E E T S E

387            396            405            414            423            432

ATA ATT GAA CAG ATC CCT GCT TCA GAA AAC AAT GTG GAA GAA ATG GTA CAG CCT  
-----  
I I E Q I P A S E N N V E E M V Q P

FIG.11A

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441 450 459 .. 468 477 486  
GCT GAG TCC CAG GCT AAT GAT GTT GGC TTC AAG AAA GTA TTT AAA TTT GTT GGT  
-----  
A E S Q A N D V G F K K V F K F V G

495 504 513 522 531 540  
TTT AAA TTC ACG GTG AAG AAG GAT AAA AAT GAA AAG TCA GAT ACT GTC CAA CTA  
-----  
F K F T V K K D K N E K S D T V Q L

549 558 567 576 585 594  
CTC ACT GTC AAG AAG GAT GAA GGC GAA GGG GCA GAA GCC TCT GTC GGA GCT GGA  
-----  
L T V K K D E G E G A E A S V G A G

603 612 621 630 639 648  
GAC CAC CAG GAG CCC AGT GTG GAG ACT GCC GTC GGA GAG TCA GCA TCC AAA GAA  
-----  
D H Q E P S V E T A V G E S A S K E

657 666 675 684 693 702  
AGT GAG CTG AAG CAA TCC ACA GAG AAG CAA GAA GGC ACC CTG AAG CAA GAA CAG  
-----  
S E L K Q S T E K Q E G T L K Q E Q

711 720 729 738 747 756  
AGC AGC ACA GAA ATC CCC CTT CAA GCC GAA TCT GAT CAA GCG GCT GAG GAA GAA  
-----  
S S T E I P L Q A E S D Q A A E E E

765 774 783 792 801 810  
GCC AAA GAT GAA GGA GAA AAA CAA GAG AAA GAG CCC ACC AAG TCC CCA GAA  
-----  
A K D E G E E K Q E K E P T K S P E

819 828 837 846 855 864  
TCC CCG AGC AGC CCA GTC AAC AGT GAG ACA ACA TCT TCC TTC AAG AAG TTC TTC  
-----  
S P S S P V N S E T T S S F K K F F

FIG.11B

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873	882	891	900	909	918												
ACT	CAC	GGT	TGG	GCC	GGC	TGG	CGC	AAG	AAG	ACC	AGC	TTC	AAG	AAA	TCA	AAA	GAG
- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -
T	H	G	W	A	G	W	R	K	K	T	S	F	K	K	S	K	E
927	936	945	954	963	972												
GAT	GAT	CTG	GAA	ACT	GCC	GAG	AAG	AGA	AAG	GAG	CAA	GAG	GCA	GAA	AAA	GTA	GAC
- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	
D	D	L	E	T	A	E	K	R	K	E	Q	E	A	E	K	V	D
981	990	999	1008	1017	1026												
GAG	GAA	GAA	AAG	GAA	AAG	ACA	GAG	CCA	GCC	TCG	GAG	CAG	GAG	CCG	GCA	GAA	
- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	
E	E	E	K	E	K	T	E	P	A	S	E	E	Q	E	P	A	E
1035	1044	1053	1062	1071	1080												
GAC	ACA	GAC	CAG	GCC	AGG	TTG	TCA	GCA	GAC	TAC	GAG	AAG	GTG	GAG	CTG	CCT	TTG
- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	
D	T	D	Q	A	R	L	S	A	D	Y	E	K	V	E	L	P	L
1089	1098	1107	1116	1125	1134												
GAA	GAC	CAG	GTT	GGT	GAC	CTG	GAG	GCA	TCG	TCA	GAG	GAG	AAG	TGT	GCT	CCT	TTG
- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	
E	D	Q	V	G	D	L	E	A	S	S	E	E	K	C	A	P	L
1143	1152	1161	1170	1179	1188												
GCA	ACG	GAA	GTG	TTT	GAT	GAG	AAG	ATG	GAA	GCC	CAC	CAA	GAA	GTT	GTT	GCA	GAG
- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	
A	T	E	V	F	D	E	K	M	E	A	H	Q	E	V	V	A	E
1197	1206	1215	1224	1233	1242												
GTC	CAC	GTG	AGC	ACC	GTG	GAG	AAG	ACA	GAG	GAG	CAG	GGA	GGA	GGA	GGA	GAG	
- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	
V	H	V	S	T	V	E	K	T	E	E	E	Q	G	G	G	G	E
1251	1260	1269	1278	1287	1296												
GCT	GAA	GGG	GGC	GTG	GTG	GTA	GAA	GGA	ACA	GGA	GAA	TCC	TTG	CCC	CCT	GAG	AAA
- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	- - -	
A	E	G	G	V	V	V	E	G	T	G	E	S	L	P	P	E	K

FIG.11C

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1305 1314 1323 .. 1332 1341 1350  
CTG GCT GAG CCC CAG GAG GTC CCC CAG GAA GCT GAG CCT GCT GAG GAG CTG ATG  
-----  
L A E P Q E V P Q E A E P A E E L M

1359 1368 1377 1386 1395 1404  
AAG AGC AGA GAG ATG TGT GTC TCT GGA GGA GAC CAC ACT CAA CTG ACA GAC CTA  
-----  
K S R E M C V S G G D H T Q L T D L

1413 1422 1431 1440 1449 1458  
AGT CCT GAA GAG AAG ACG CTG CCC AAA CAC CCA GAA GGC ATT GTC AGT GAG GTG  
-----  
S P E E K T L P K H P E G I V S E V

1467 1476 1485 1494 1503 1512  
GAG ATG CTG TCC TCT CAG GAA AGA ATC AAG GTA CAG GGA AGT CCC TTG AAG AAA  
-----  
E M L S S Q E R I K V Q G S P L K K

1521 1530 1539 1548 1557 1566  
CTC TTC AGT AGC TCA GGC TTA AAG AAG CTG TCT GGG AAG AAG CAG AAG GGG AAA  
-----  
L F S S S G L K K L S G K K Q K G K

1575 1584 1593 1602 1611 1620  
CGA GGA GGT GGG GGA GAC GAA GAG CCT GGA GAA TAC CAA CAC ATT CAC ACC GAA  
-----  
R G G G G D E E P G E Y Q H I H T E

1629 1638 1647 1656 1665 1674  
TCC CCA GAG AGT GCT GAT GAG CAG AAG GGA GAG AGC TCT GCG TCG TCC CCC GAG  
-----  
S P E S A D E Q K G E S S A S S P E

1683 1692 1701 1710 1719 1728  
GAG CCT GAG GAG ACC ACG TGT CTG GAG AAA GGG CCG CTG GAA GCA CCC CAG GAT  
-----  
E P E E T T C L E K G P L E A P Q D

FIG.11D

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1737	1746	1755	1764	1773	1782
GGG GAA GCT GAG GAA GGA ACT ACT	TCC GAT GGA GAG AAG AAG AGA GAA GGG ATC				
G E A E E G T T S D G E K K R E G I					
1791	1800	1809	1818	1827	1836
ACT CCC TGG GCA TCC TTC AAA AAG ATG GTG ACA CCC AAG AAA CGG GTC CGA AGA					
T P W A S F K K M V T P K K R V R R					
1845	1854	1863	1872	1881	1890
CCT TCT GAG AGT GAC AAG GAG GAA GAG CTG GAG AAG GTC AAG AGC GCC ACC TTG					
P S F S D K E E E L E K V K S A T L					
1899	1908	1917	1926	1935	1944
TCC TCC ACT GAT AGC ACA GTG TCA GAA ATG CAA GAT GAA GTC AAA ACT GTT GGT					
S S T D S T V S E M Q D E V K T V G					
1953	1962	1971	1980	1589	1998
GAG GAA CAA AAG CCA GAG GAA CCA AAG CGT AGG GTG GAT ACT TCA GTG TCT TGG					
E E Q K P E E P K R R V D T S V S W					
2007	2016	2025	2034	2043	2052
GAA GCA CTG ATT TGT GTC GGA TCA TCC AAG AAG AGA GCA AGG AAG GCA TCC TCT					
E A L I C V G S S K K R A R K A S S					
2061	2070	2079	2088	2097	2106
TCA GAT GAT GAA GGA GGG CCA AGG ACA CTG GGA GGG GAC AGT CAC AGA GCA GAG					
S D D E G G P R T L G G D S H R A E					
2115	2124	2133	2142	2151	2160
GAG GCC AGC AAA GAC AAA GAA GCC GGA ACA GAC GCT GTT CCT GCC AGC ACC CAG					
E A S K D K E A G T D A V P A S T Q					

FIG.11E

( 24 of 90 )

2169 2178 2187 2196 2205 2114  
GAG CAG GAC CAA GCG CAA GGA AGT ICC TCA CCC GAG CCA GCG GGA AGC CTT TCC  
-----  
E Q D Q A Q G S S S P E P A G S P S

2223 2232 2241 2250 2259 2268  
GAA GGG GAA GGT GTC TCC ACT TGG GAG TCA TTT AAA AGA TTA GTC ACT CCA AGA  
-----  
E G E G V S T W E S F K R L V T P R

2277 2286 2295 2304 2313 2322  
AAA AAA TCC AAG TCA AAA CTG GAA GAG AAA GCC GAA GAC TCT AGT GTA GAG CAG  
-----  
K K S K S K L E E K A E D S S V E Q

2331 2340 2349 2358 2367 2376  
TTG TCC ACT GAG ATC GAA CCG AGT AGA GAA GAA TCT TGG GTT TCC ATT AAG AAA  
-----  
L S T E I E P S R E E S W V S I K K

2385 2394 2403 2412 2421 2430  
TTC ATC CCC GGA CGG CGG AAG AAA AGG GCA GAC GGG AAG CAA GAA CAA GCC ACT  
-----  
F I P G R R K K R A D G K Q E Q A T

2439 2448 2457 2466 2475 2484  
GTG GAA GAC TCA GGG CCA GTG GAG ATA AAT GAG GAC GAC CCT AAT GTC CCA GCC  
-----  
V E D S G P V E I N E D D P N V P A

2493 2502 2511 2520 2529 2538  
GTC GTG CCT CTG TCT GAG TAT AAT GCA GTG GAG AGG GAG AAG ATG GAA GCC CAG  
-----  
V V P L S E Y N A V E R E K M E A Q

2547 2556 2565 2574 2583 2592  
GGG AAT ACG GAG CTG CCC CAG CTG CTG GGG GCT GTG TAC GTG TCC GAG GAG CTC  
-----  
G N T E L P Q L L G A V Y V S E E L

FIG.11F

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2601	2610	2619	2628	2637	2646												
AGT	AAG	ACT	CTG	GTC	CAC	ACT	GTG	AGT	GTC	GCA	GTC	ATT	GAT	GGG	ACC	AGG	GCA
- - - - -																	
S	K	T	L	V	H	T	V	S	V	A	V	I	D	G	T	R	A
2655	2664	2673	2682	2691	2700												
GTC	ACC	AGT	GTC	GAA	GAG	CGG	TCT	CCT	TCG	TGG	ATA	TCC	GCT	TCC	GTA	ACA	GAA
- - - - -																	
V	T	S	V	E	E	R	S	P	S	W	I	S	A	S	V	T	E
2790	2718	2727	2736	2745	2754												
CCT	CTT	GAA	CAC	ACA	GCG	GGA	GAA	GCC	ATG	CCA	CCT	GTT	GAA	GAG	GTC	ACT	GAA
- - - - -																	
P	L	E	H	T	A	G	E	A	M	P	P	V	E	E	V	T	E
2763	2772	2781	2790	2799	2808												
AAA	GAC	ATC	ATT	GCA	GAA	GAA	ACT	CCT	GTG	CTC	ACC	CAG	ACG	TTA	CCA	GAG	GGT
- - - - -																	
K	D	I	I	A	E	E	T	P	V	L	T	Q	T	L	P	E	G
2817	2826	2835	2844	2853	2862												
AAA	GAT	GCC	CAT	GAC	GAC	ATG	GTC	ACC	AGT	GAA	GTG	GAT	TTC	ACC	TCA	GAA	GCT
- - - - -																	
K	D	A	H	D	D	M	V	T	S	E	V	D	F	T	S	E	A
2871	2880	2889	2898	2907	2916												
GTG	ACA	GCC	ACA	GAG	ACC	TCA	GAG	GCT	CTC	CGT	ACT	GAA	GAA	GTT	ACC	GAA	GCA
- - - - -																	
V	T	A	T	E	T	S	E	A	L	R	T	E	E	V	T	E	A
2925	2934	2943	2952	2961	2970												
TCG	GGG	GCC	GAA	GAG	ACC	ACA	GAC	ATG	GTG	TCC	GCA	GTT	TCC	CAG	CTG	ACT	GAC
- - - - -																	
S	G	A	E	E	T	T	D	M	V	S	A	V	S	Q	L	T	D
2979	2988	2997	3006	3015	3024												
TCC	CCA	GAC	ACC	ACA	GAG	GAA	GCC	ACC	CCA	GTT	CAG	GAG	GTA	GAG	AGT	GGT	GTG
- - - - -																	
S	P	D	T	T	E	E	A	T	P	V	Q	E	V	E	S	G	V

FIG.11G

3033	3042	3051	3060	3069	3078
CTA GAT ACA GAA GAA GAG GAG CGC CAG ACG CAG GCC ATC CTC CAA GCC GTT GCA					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
L D T E E E R Q T Q A I L Q A V A					
3087	3096	3105	3114	3123	3132
GAC AAG GTG AAA GAG GAG TCC CAG GTG CCT GCA ACC CAG ACT GTG CAG AGA ACG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
D K V K E E S Q V P A T Q T V Q R T					
3141	3150	3159	3168	3177	3186
GGG TCA AAA GCA CTG GAG AAG GTT GAG GAG GTA GAG GAG GAC TCC GAA GTG CTG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
G S K A L E K V E E V E E D S E V L					
3195	3204	3213	3222	3231	3240
GCT TCG GAG AAA GAG AAG GAC GTT ATG CCG AAA GGA CCC GTG CAG GAA GCT GGA					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
A S E K E K D V M P K G P V Q E A G					
3195	3258	3267	3276	3285	3294
GCT GAG CAT CTT GCA CAG GGC TCT GAG ACT GGA CAG GCT ACT CCA GAG AGC CTT					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
A E H L A Q G S E T G Q A T P E S L					
3303	3312	3321	3330	3339	3348
GAA GTT CCT GAA GTC ACG GCA GAT GTA GAC CAT GTC GCC ACG TGC CAG GTT ATC					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
E V P E V T A D V D H V A T C Q V I					
3357	3366	3375	3384	3393	3402
AAG CTC CAG CAG CTG ATG GAA CAG GCC GTG GCC CCT GAG TCA TCC GAA ACC TTG					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
K L Q Q L M E Q A V A P E S S S E T L					
3411	3420	3429	3438	3447	3456
ACA GAC AGT GAG ACA AAT GGA AGC ACT CCC TTA GCA GAT TCA GAC ACT GCA GAT					
- - - - -	- - - - -	- - - - -	- - - - -	- - - - -	- - - - -
T D S E T N G S T P L A D S D T A D					

FIG.11H

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3465	3474	3483	3492	3501	3510
GGG ACA CAG CAA GAT GAA ACC ATT GAC AGC CAG GAC AGT AAA GCC ACT GCA GCT					
-----					
G	T	Q	Q	D	A
3519	3528	3537	3546	3555	3564
GTC AGG CAG TCA CAG GTC ACA GAA GAA GAG GCG GCT ACT GCT CAG AAA GAG GAG					
-----					
V	R	Q	S	Q	E
3573	3582	3591	3600	3609	3618
CCT TCG ACA CTA CCT AAT AAT GTT CCA GCC CAG GAA GAA CAT GGG GAA GAA CCA					
-----					
P	S	T	L	P	P
3627	3636	3645	3654	3663	3672
GGA AGA GAT GTT CTT GAA CCT ACA CAG CAA GAG CTT ACT GCT GCA GCC GTG CCC					
-----					
G	R	D	V	L	P
3681	3690	3699	3708	3717	3726
GTT CTG GCA AAG ACT GAG GTG GGT CAA GAG GGT GAG GTT GAC TGG TTG GAT GGA					
-----					
V	L	A	K	T	E
3735	3744	3753	3762	3771	3780
GAA AAA GTC AAA GAA GAA CAG GAG GTG TTT GTA CAC TCT GGA CCC AAC AGT CAA					
-----					
E	K	V	K	E	E
3789	3798	3807	3816	3825	3834
AAG GCT GCT GAT GTG ACA TAT GAC AGT GAA GTG ATG GGA GTG GCC GGG TGT CAG					
-----					
K	A	A	D	V	T
3843	3852	3861	3870	3879	3888
GAA AAG GAG AGT ACT GAA GTG CAG AGT CTT AGC CTG GAG GAG GGA GAG ATG GAA					
-----					
E	K	E	S	T	E

FIG.111

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3897        3906        3915        3924        3933        3942  
ACT GAC GTT GAA AAG GAG AAA AGG GAG ACA AAG CCA GAG CAA GTG AGT GAA GAA  
-----  
T D V E K E K R E T K P E Q V S E E

3951        3960        3969        3978        3987        3996  
GGT GAG CAG GAA ACA GCC GCT CCT GAG CAT GAA GGA ACC TAC GGG AAG CCA GTC  
-----  
G E Q E T A A P E H E G T Y G K P V

4005        4014        4023        4032        4041        4050  
CTG ACA CTT GAC ATG CCC AGC TCA GAG AGG GGG AAG GCA CTG GGA AGC CTT GGA  
-----  
L T L D M P S S E R G K A L G S L G

4059        4068        4077        4086        4095        4104  
GGA AGC CCT TCT CTC CCA GAC CAA GAC AAA GCA GGT TGC ATA GAG GTT CAA GTT  
-----  
G S P S L P D Q D K A G C I E V Q V

4113        4122        4131        4140        4149        4158  
CAA AGC CTG GAC ACA ACA GTC ACT CAA ACA GCA GAA GCT GTG GAA AAG GTC ATA  
-----  
Q S L D T T V T Q T A E A V E K V I

4167        4176        4185        4194        4203        4212  
GAA ACG GTT GTG ATT TCA GAG ACA GGT GAA AGT CCA GAG TGT GTA GGT GAC CAC  
-----  
E T V V I S E T G E S P E C V G A H

4221        4230        4239        4248        4257        4266  
TTA TTA CCA GCT GAG AAG TCC TCT GCA ACG GGT GGC CAC TGG ACT CTT CAG CAT  
-----  
L L P A E K S S A T G G H W T L Q H

4275        4284        4293        4902        4311        4320  
GCA GAG GAC ACG GTA CCC CTG GGG CCT GAG TCT CAG GCA GAA TCC ATC CCA ATC  
-----  
A E D T V P L G P E S Q A E S I P I

FIG.11J

4329	4338	4347	4356	4365	4374
ATA GTA ACT CCT GCT CCT GAA AGC ACC CTA CAT CCT GAC CTA CAA GGA GAA ATA					
I	V	T	P	A	I
4383	4392	4401	4410	4419	4428
AGC GCA TCC CAG AGA GAG CGA TCA GAG GAA GAG GAC AAG CCA GAT GCT GGT CCT					
S	A	S	Q	R	P
4437	4446	4455	4464	4473	4482
GAT GCT GAC GGC AAG GAG AGT ACA GCA ATC GAA AAA GTC CTC AAG GCT GAA CCT					
D	A	D	G	K	P
4491	4500	4509	4518	4527	4536
GAG ATC CTG GAA CTT GAG AGT AAG AGC AAC AAG ATT GTG CTG AAC GTC ATT CAG					
E	I	L	E	S	Q
4545	4554	4563	4572	4581	4590
ACA GCC GTT GAC CAG TTC GCA CGT ACA GAA ACA GCC CCC GAA ACT CAT GCT TAT					
T	A	V	D	Q	Y
4599	4608	4617	4626	4635	4644
GAT TCA CAG ACC CAG GTT CCT GCA TGC AGG CTT GAC AGC AGG GAG CCC AAC AGA					
D	S	Q	T	V	R
4653	4662	4671	4680	4689	4698
TGC TGG ACA AAA ATG AAA GAT GCC AAG ATG AAA CAC CCA GTG CCG CAG CCC AGA					
C	W	T	K	M	R
4707	4716	4725	4734	4743	4752
GAG GAC TTG CAA GTC CTG ACC GTT CTG GAG GCA TGG GCT CAG CCT CGG AAA TGC					
E	D	L	Q	V	C

FIG.11K

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4761 4770 4779 4788 4797 4806  
TTG CCG CGC TTG CAG TTG AAA GCG CCG GTG TCA AAG TAA GCA TTG AGA AGC TGC  
-----  
L P R L Q L K A P V S K \*  
  
4815 4824 4833 4842 4851 4860  
CTC CTC AAC CCA AAG ATC CAA AAG GAG CAT GCT GCT GAT GGC CCT CAG CTC CAA  
-----  
  
4869 4878 4887 4896 4905 4914  
AGC TTA GCC CAG GCA GAG GCC AGT GCC TCT GGA AAC CTA ACC AAA GAA TCC CCA  
-----  
  
4923 4932 4941 4950 4959 4968  
GAC ACC ACC GGA CCA AAG CTA ACC GAG GAG GGC GAT CCC CCA AAA GTT CAG GTC  
-----  
  
4977 4986 4995 5004 5013 5022  
CAG GAA GAA GAA ATG TCT ACC AAG TCA GTC AAA GAG AAC AAG GCC CAG GCA GAA  
-----  
  
5031 5040 5049 5058 5067 5076  
GAG GAC CTG CAG GAG CCA AAG GGA GAC CTG GCA GAA TCC TCC GAT GTT AGT TGC  
-----  
  
5085 5094 5103 5112 5121 5130  
TCA TTG TAC ATC TGT AAG ACC AGA ATG TGA AAA CAA GTC ACA GAA CAA GAT GCT  
-----  
  
5139 5148 5157 5166 5175 5184  
GCT GTT GGG ACC TTG AGA CCA AGA TTT CAG AGC CCA TGA CAT CCA GAG AGC AGG  
-----  
  
5193  
GCC GTC CAA TGA TTT C 3'

FIG.11L

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SSeCKS  
13.2.2

220 KD -



116 -

97.4 -

FIG.12

F O O T E D : E E T I E D G E D

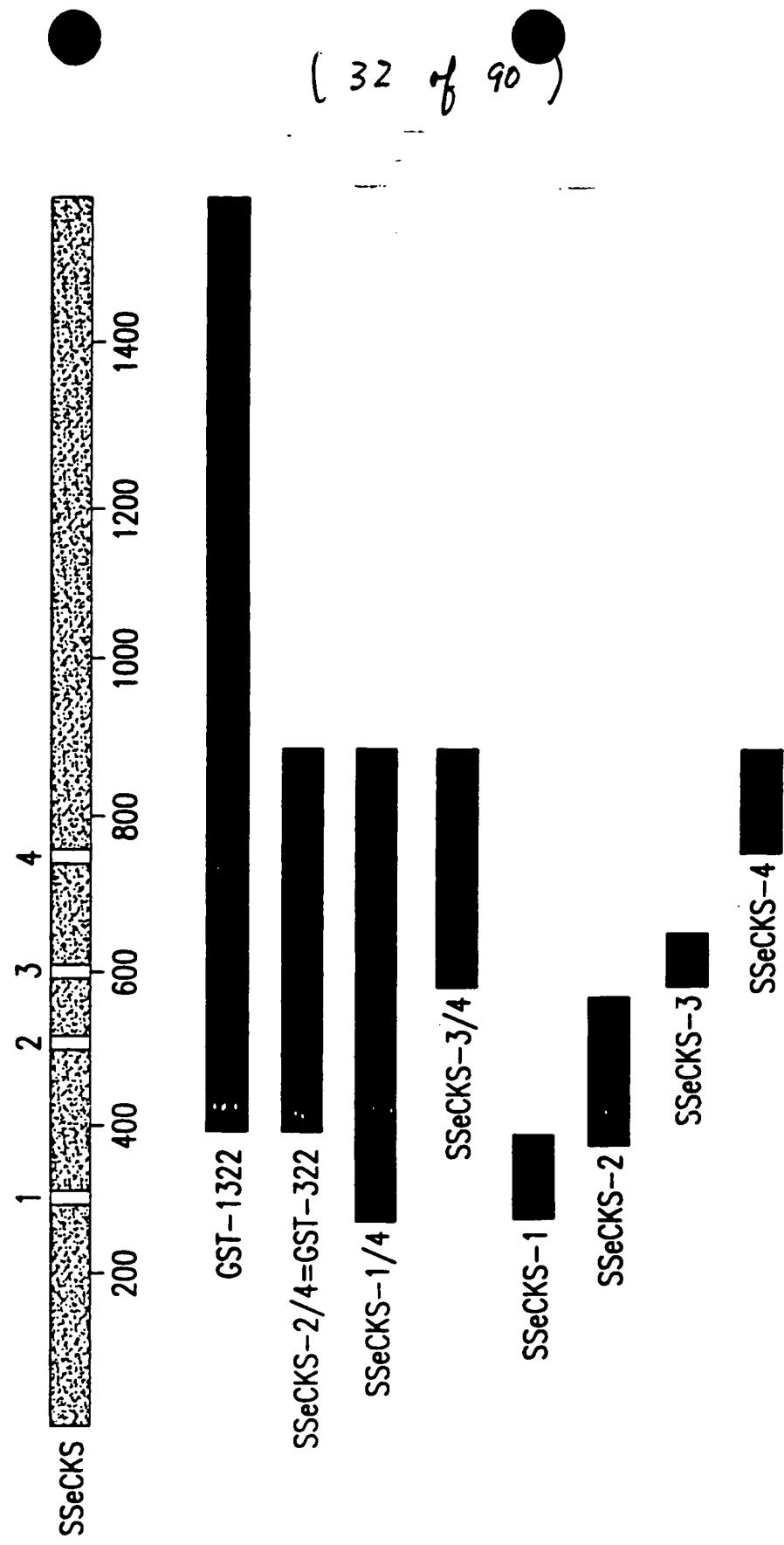


FIG. 13A

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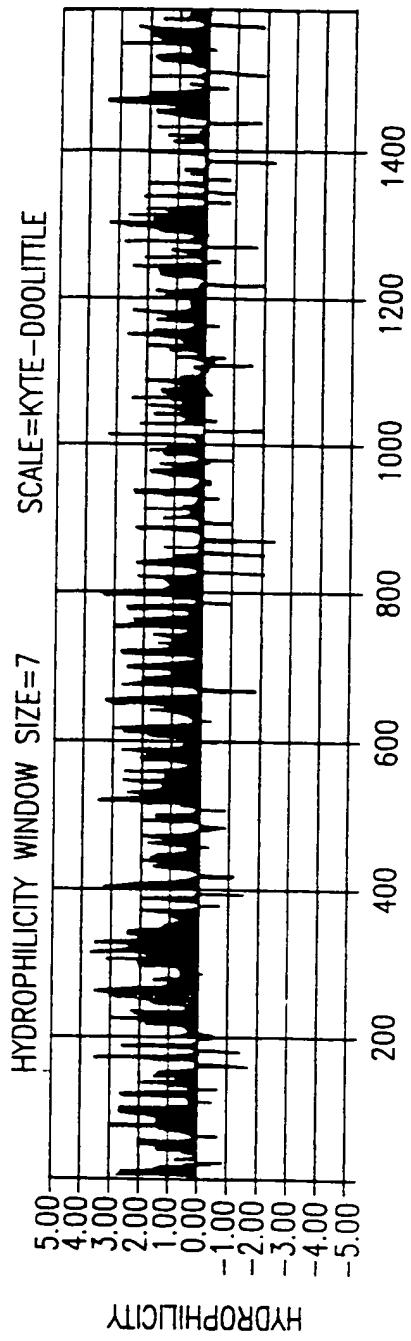


FIG. 13B



FIG. 13C

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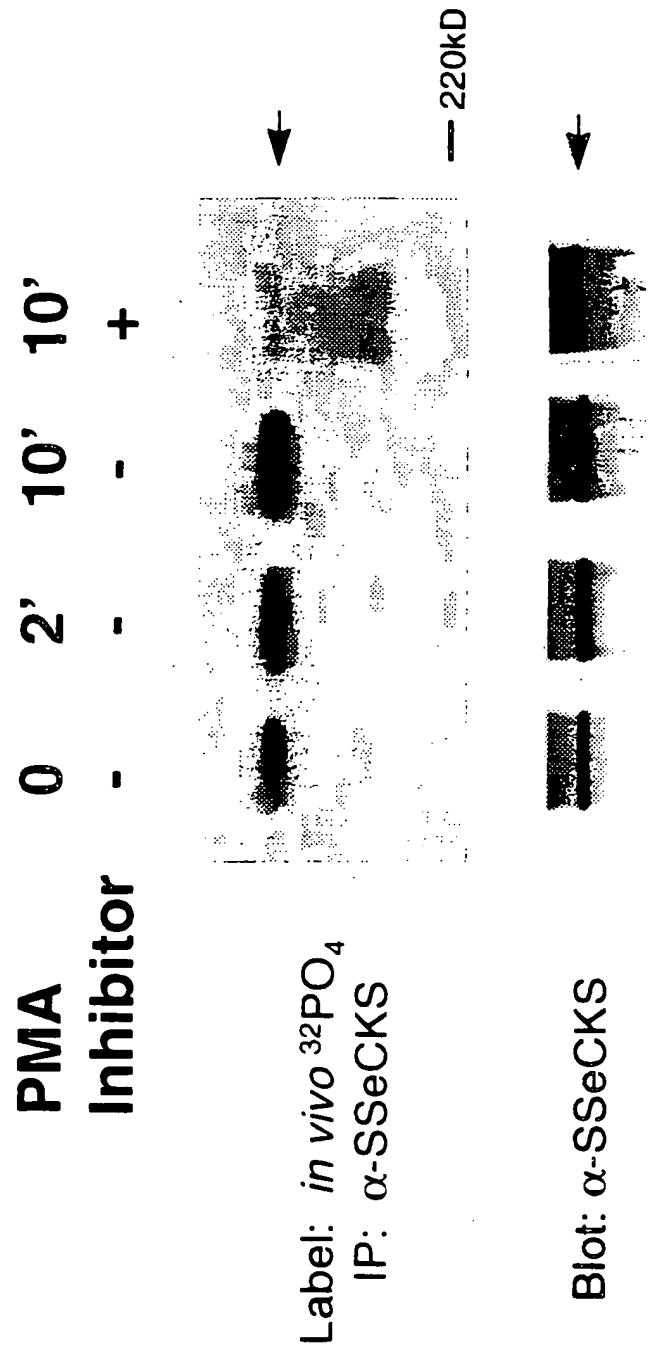


FIG. 14

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0 9 8 7 6 5 4 3 2 1 0 - +

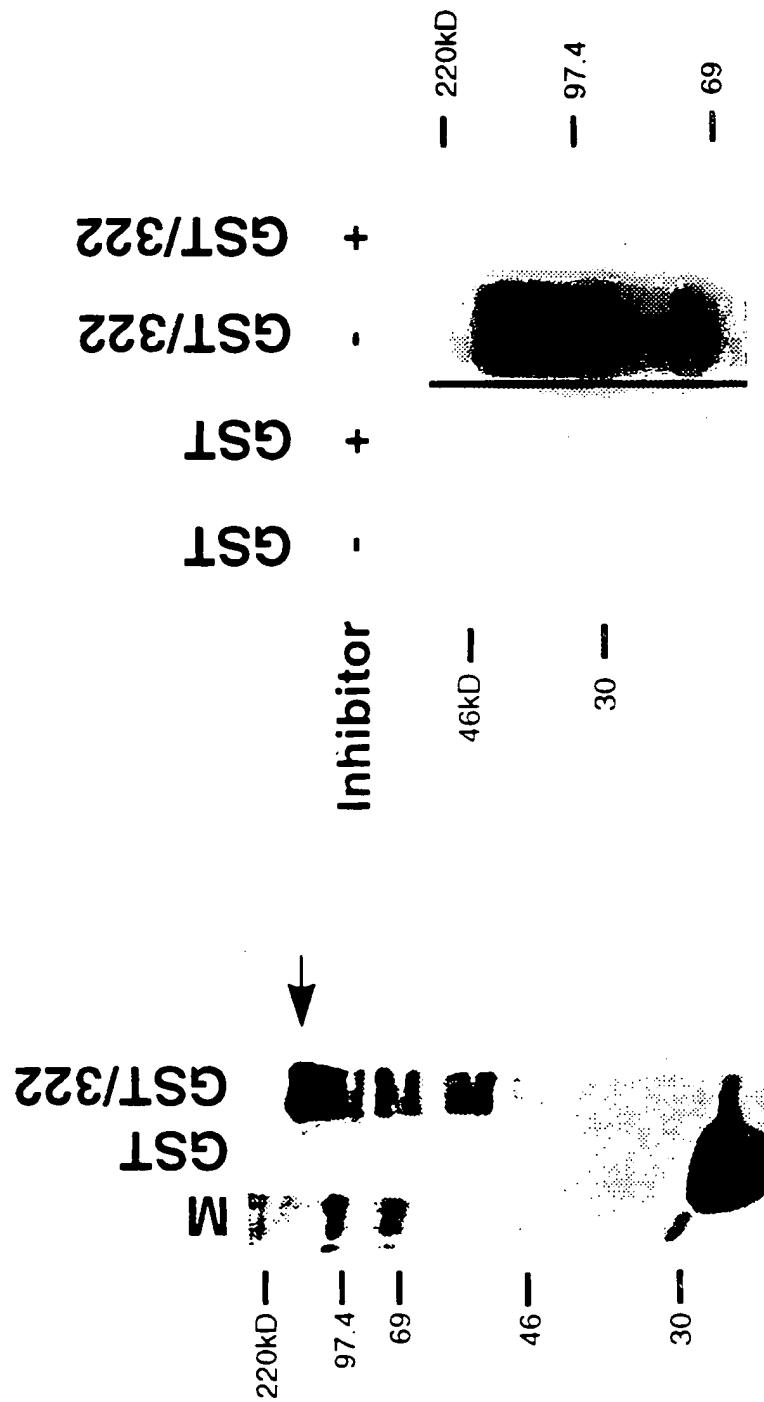


FIG. 15B

FIG. 15A

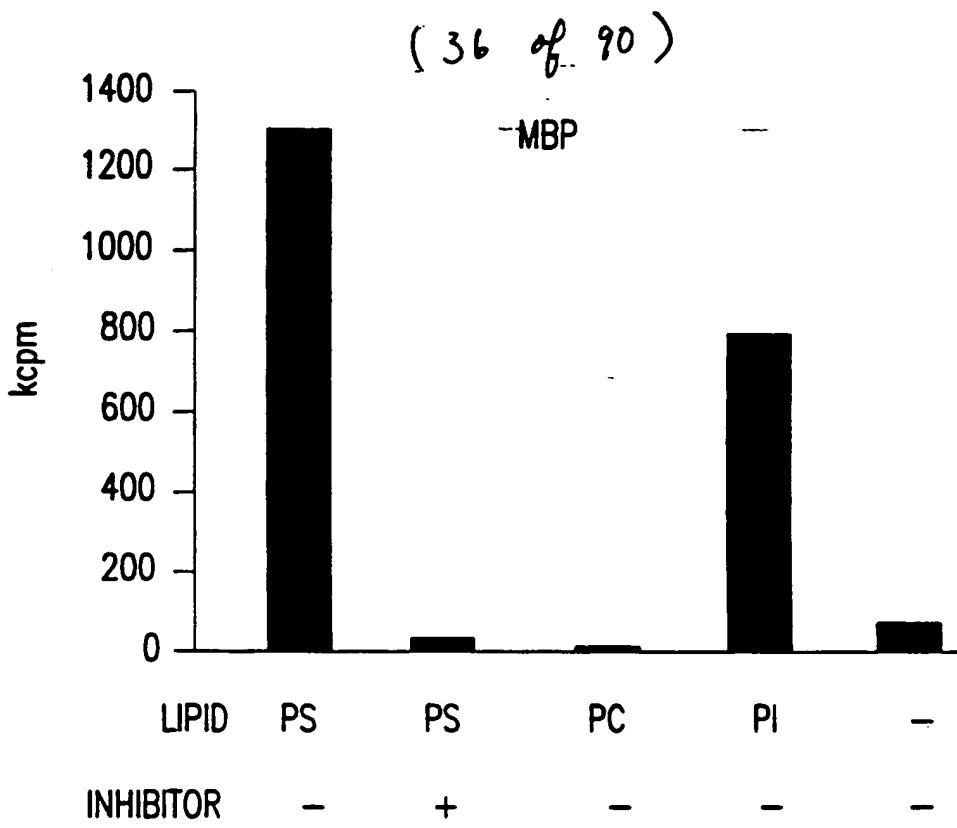


FIG.16A

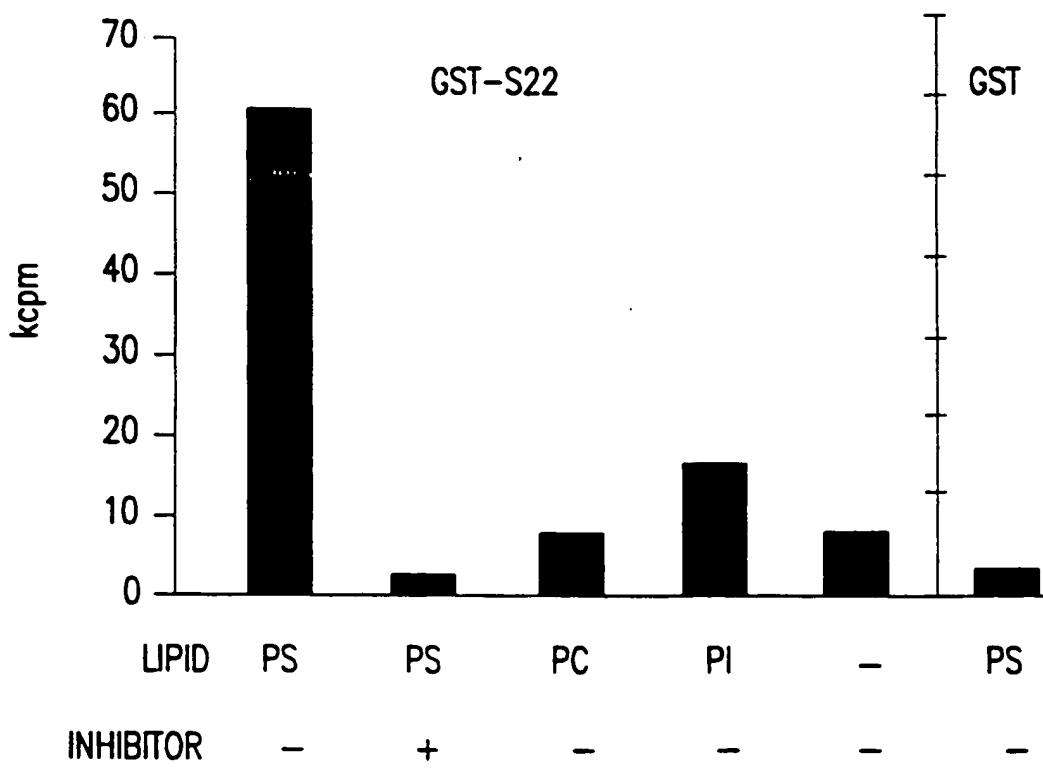


FIG.16B

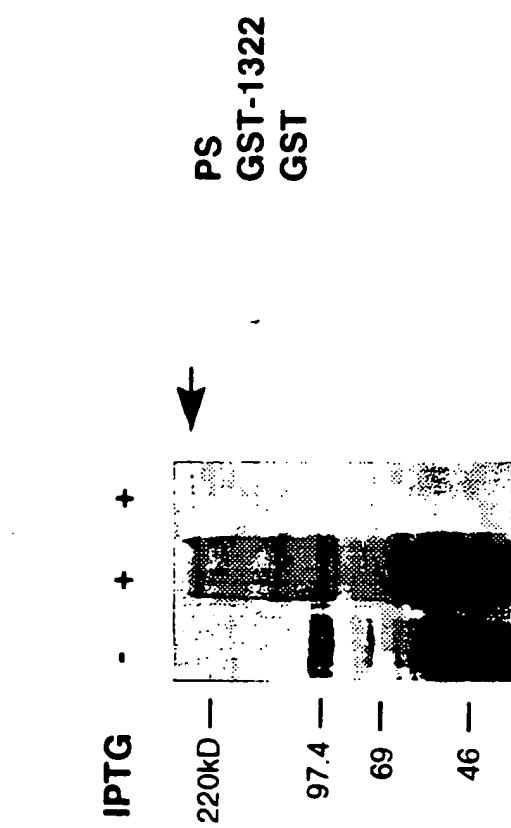


FIG. 17A

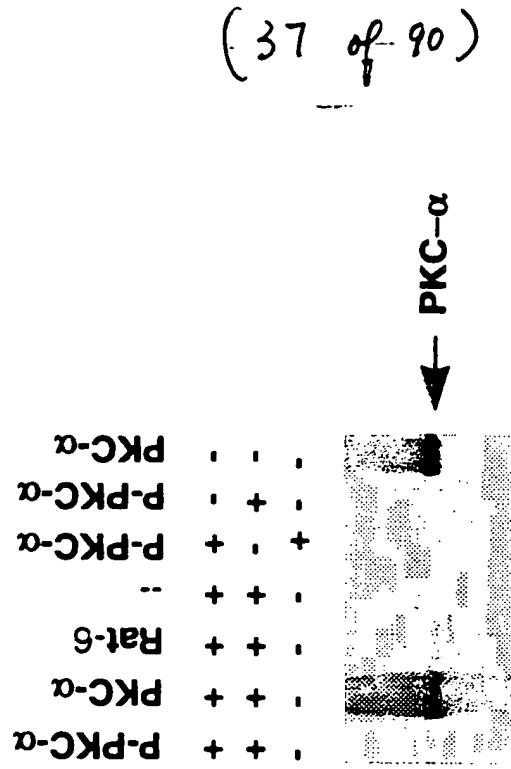


FIG. 17B

FIG. 18A

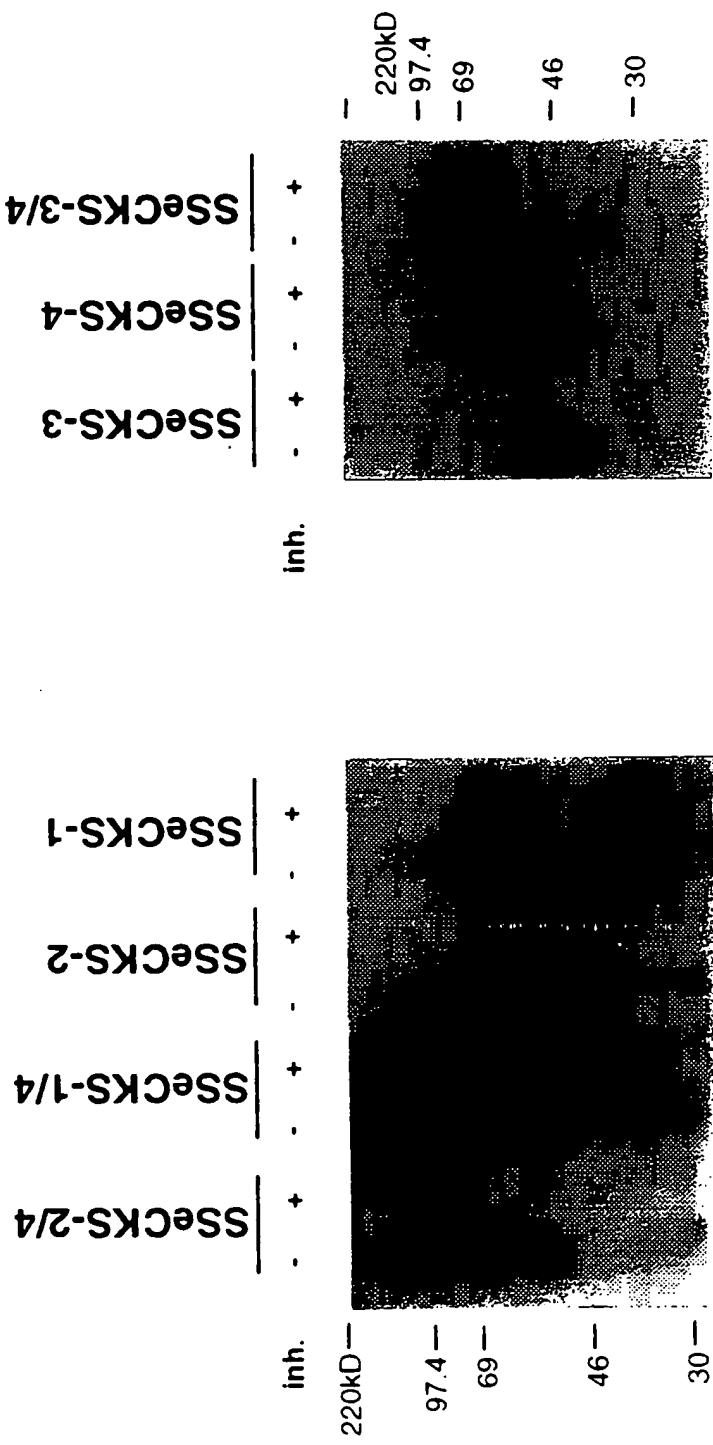
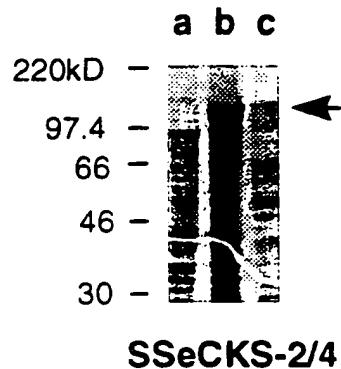


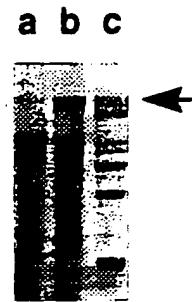
FIG. 18B

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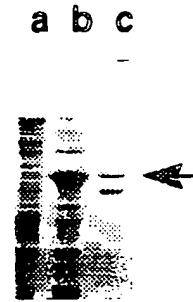
SSeCKS-2/4

FIG.18C



SSeCKS-1/4

FIG.18D



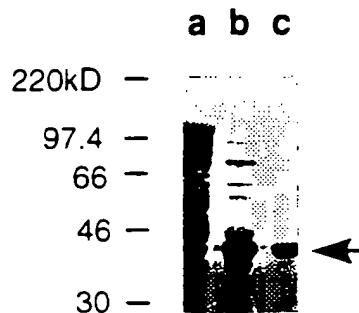
SSeCKS-2

FIG.18E



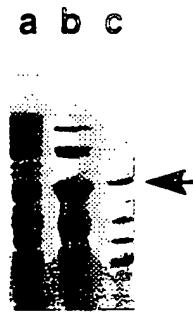
SSeCKS-1

FIG.18F



SSeCKS-3

FIG.18G



SSeCKS-4

FIG.18H



SSeCKS-3/4

FIG.18I

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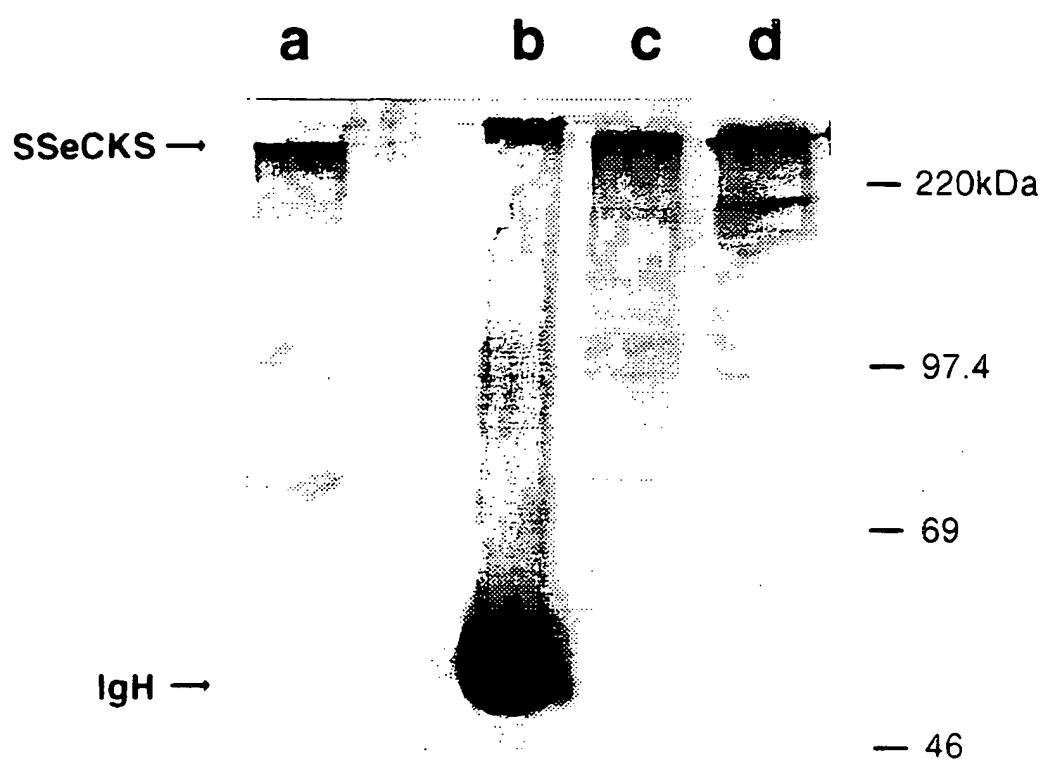


FIG. 19

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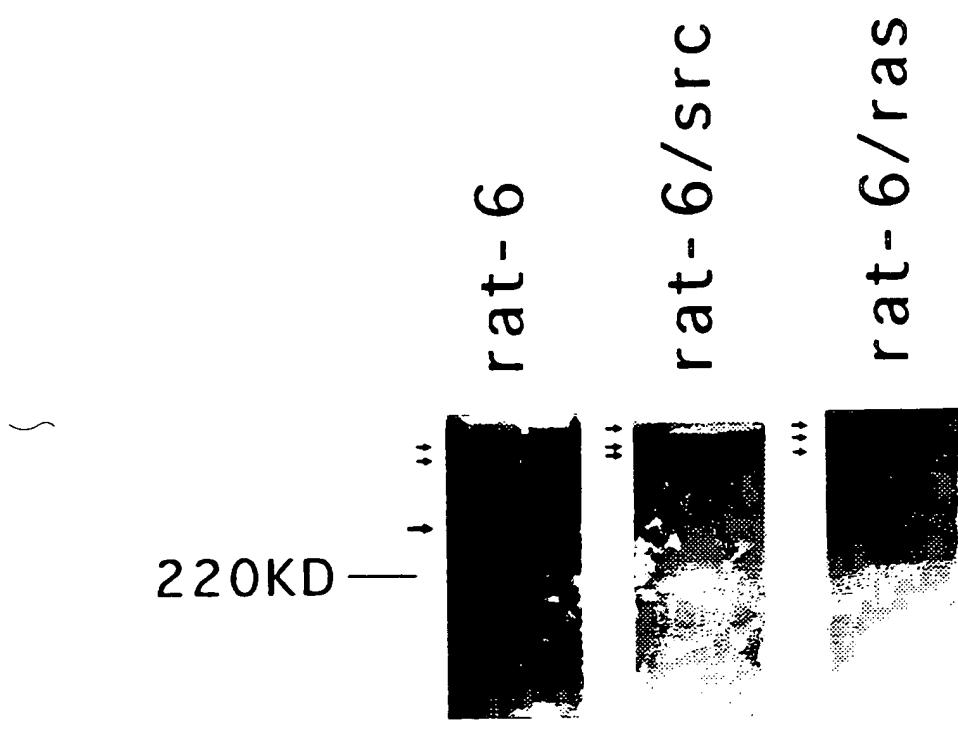


FIG.20

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FIG.21A



FIG.21B



FIG.21C



FIG.21D



FIG.21E



FIG.21F

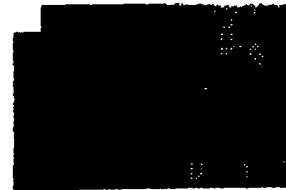


FIG.21G



FIG.21H



FIG.21I



FIG.21J

W. G. L. T. C. G. = C. C. T. H. E. G. G. G.

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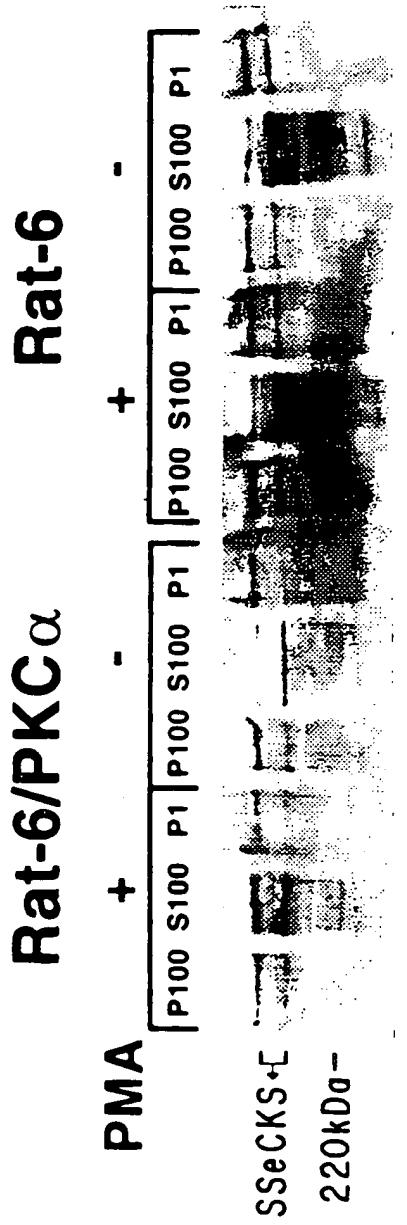


FIG. 22

( 44    80    90 )

spleen  
thymus  
prostate  
testes  
ovary  
small intestine  
colon  
PBL



FIG.23A

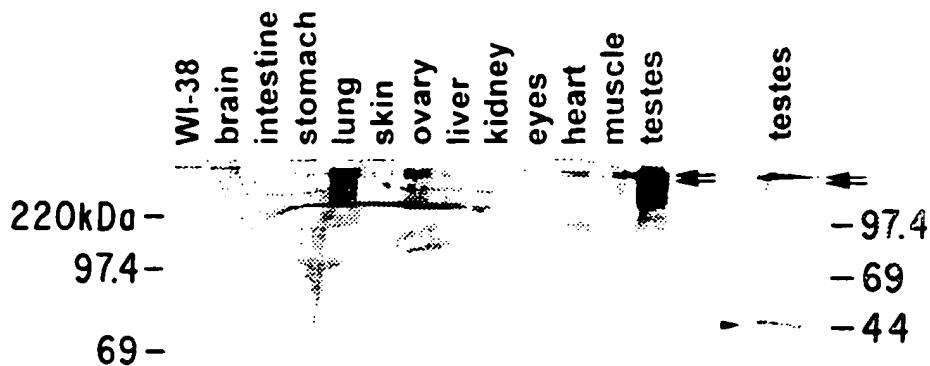


FIG.23B

(45 % 90)

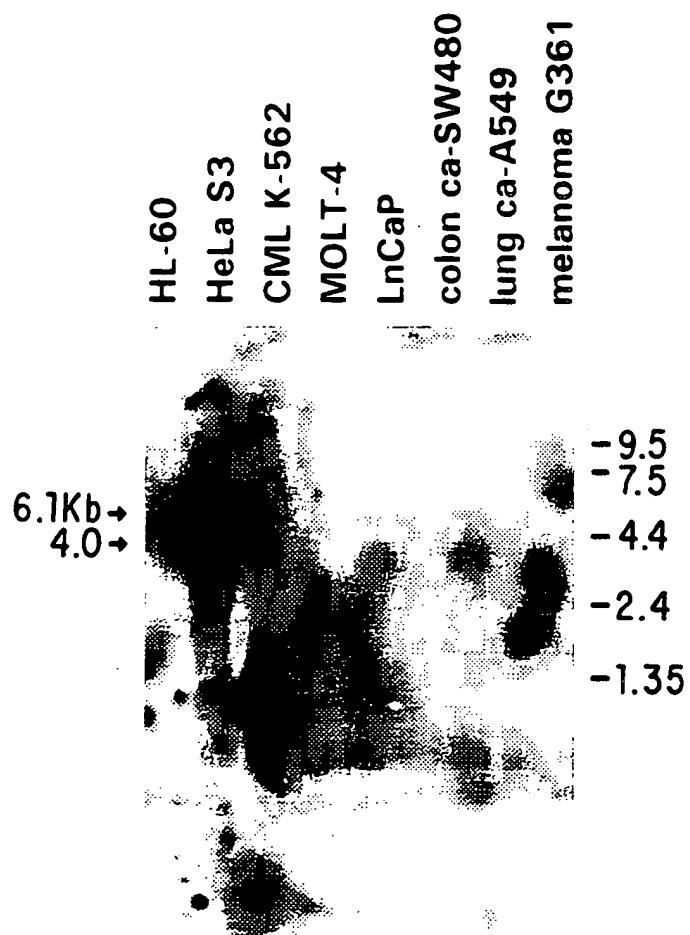


FIG.24

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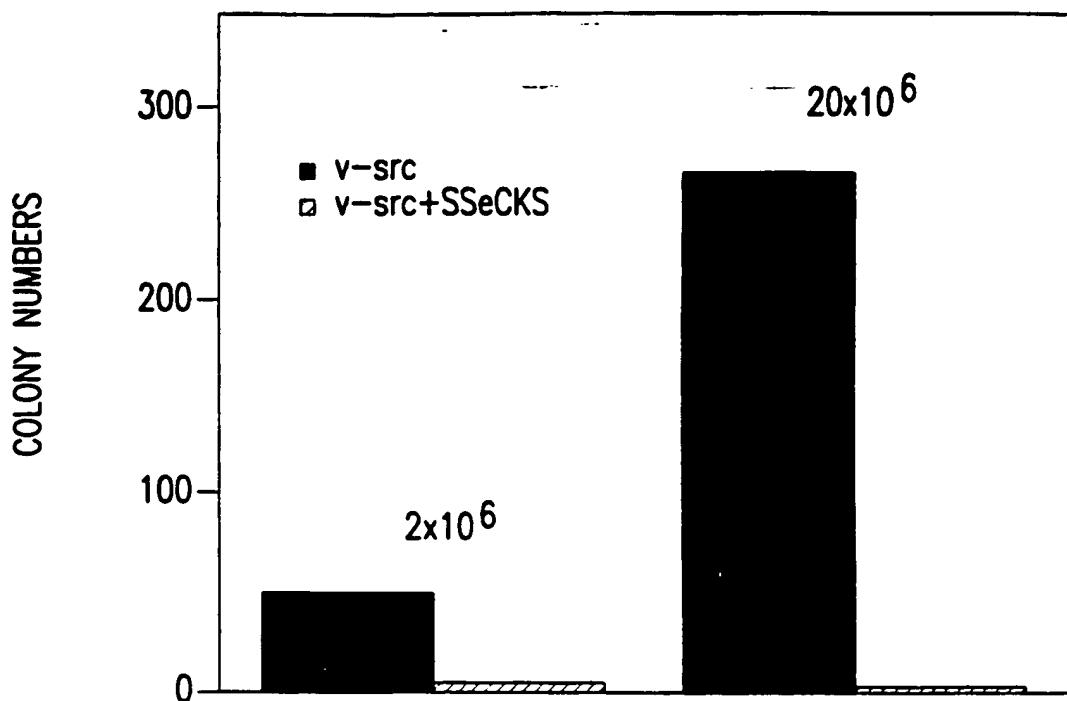


FIG.25A

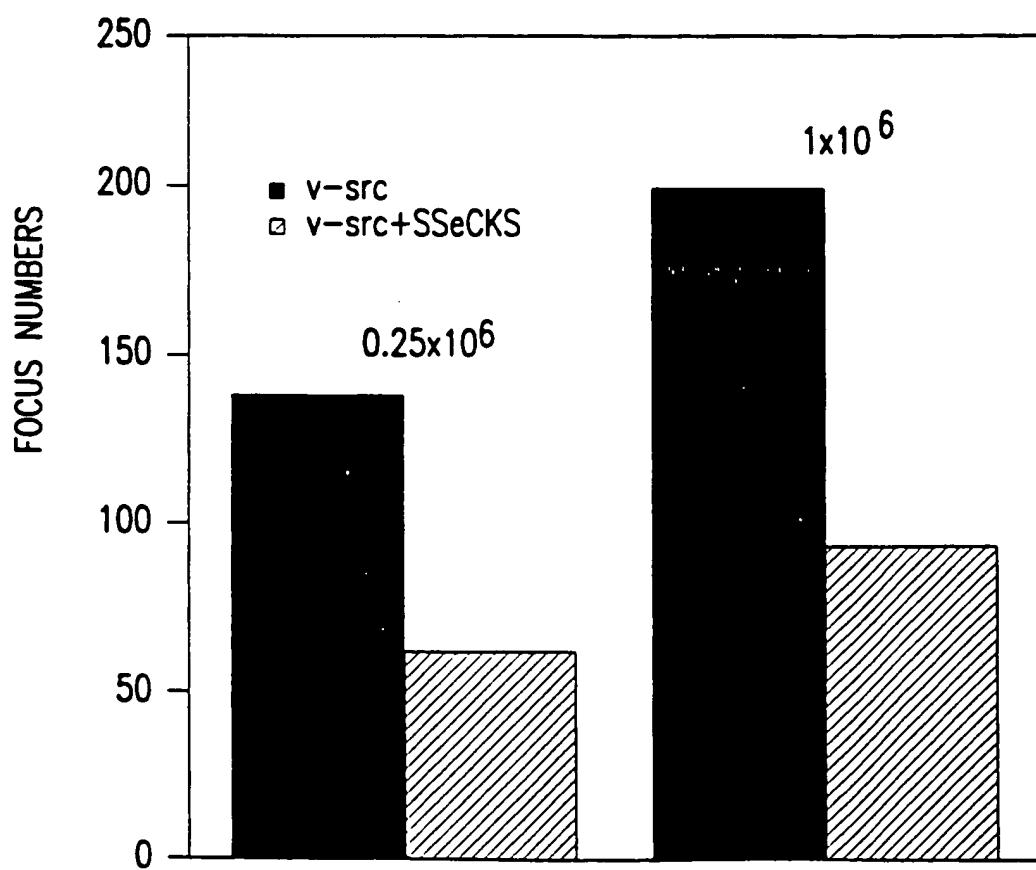


FIG.25B

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		<u>Myr.</u>	<u>Pal.</u>
src	MGSSKSKPKD	+	-
yes	MGCIKSKEDK	+	+
SSeCKS	MGAGSSTEQR	+	?
G <sub>α</sub> t1	MGAGASAEEK	+	-
G <sub>α</sub> i1	MGCTLSAEDK	+	+
GAP-43	MLCCMRRTKQ	-	+
MYRIST. CONCENSUS:	MGXXX <sub>T</sub> <sup>S</sup>		

FIG.26

(48 of 90)

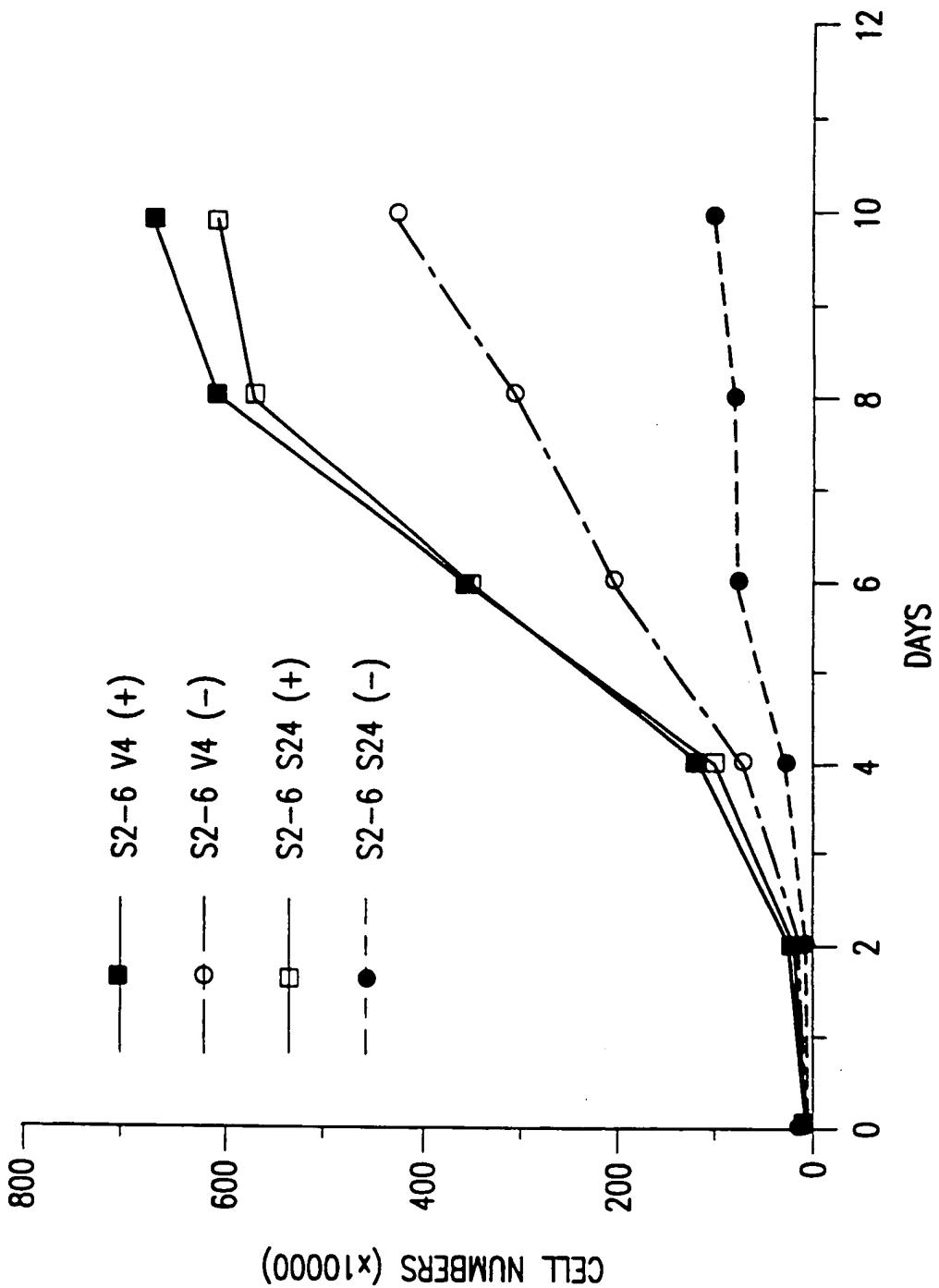


FIG.27

(49 of 90)

Tet + -



- 220kDa

FIG.28

(50 of 90)

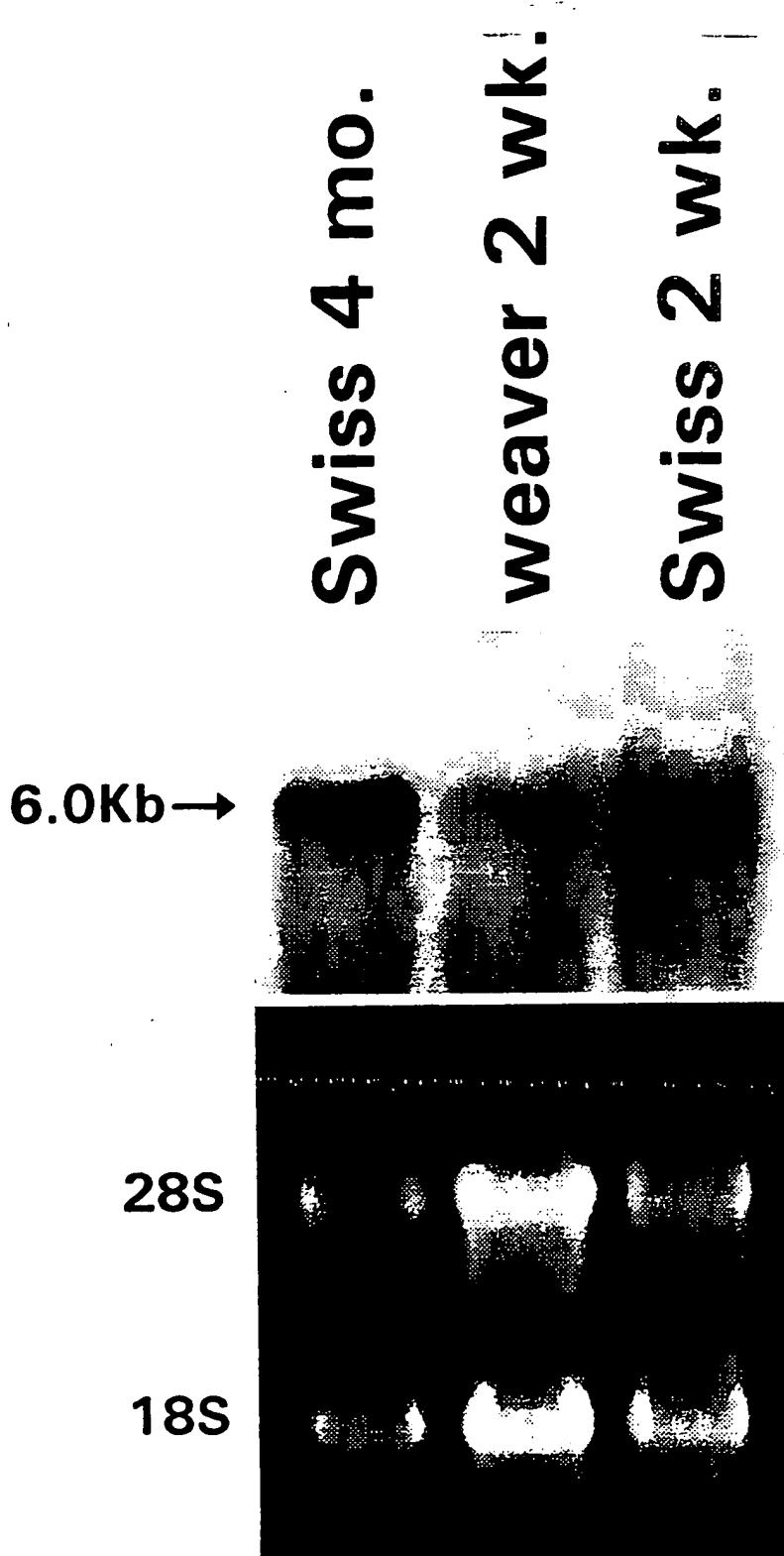


FIG. 29

(51 of 90)

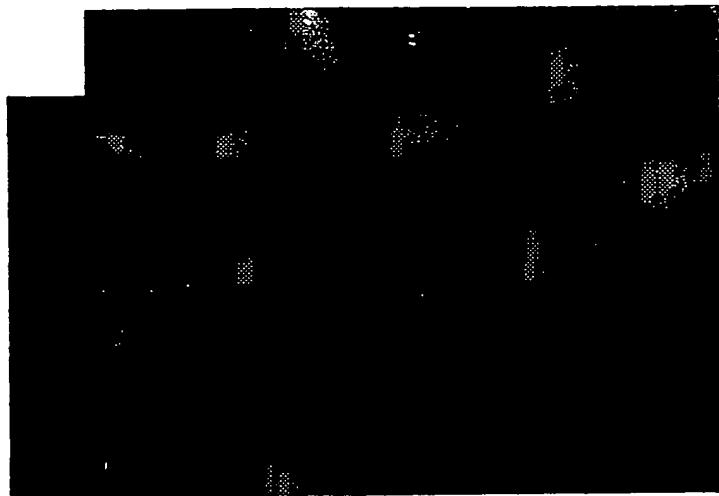


FIG.30A



FIG.30B

(52 of 90)

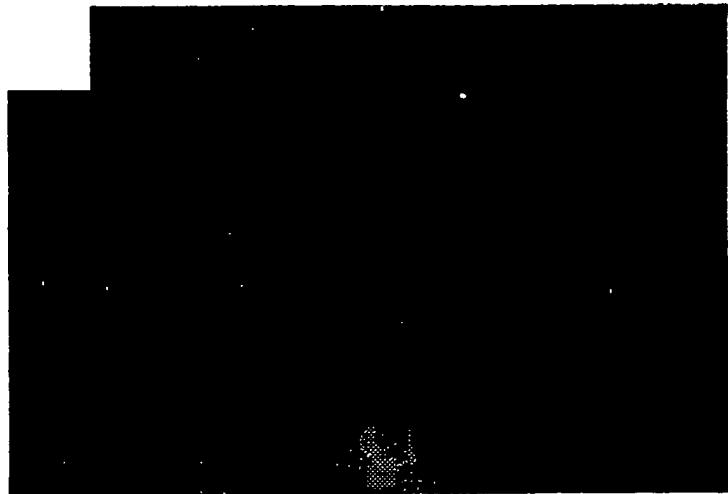


FIG.30C

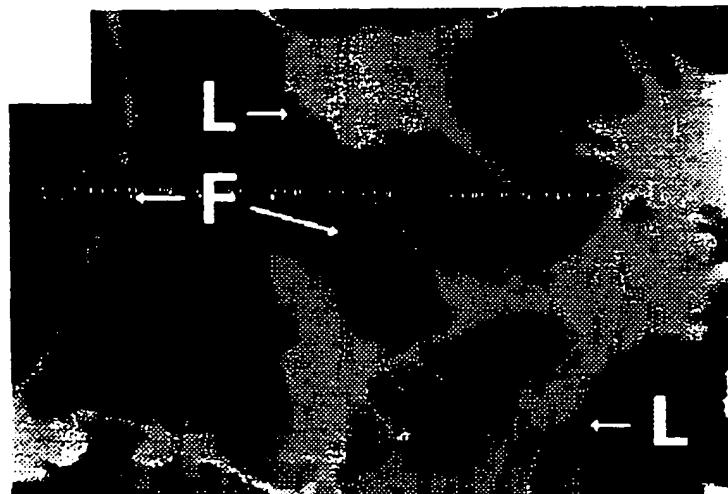


FIG.30D

(53 of 90)

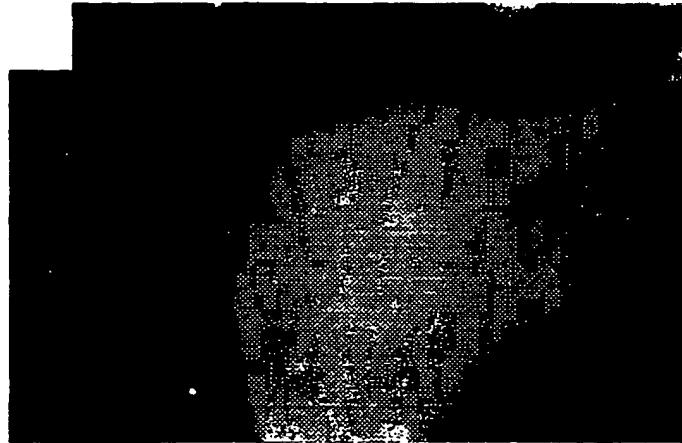


FIG.31A



FIG.31B

(54 of 90)



FIG.31C



FIG.31D

(55 of 90)



FIG.32A

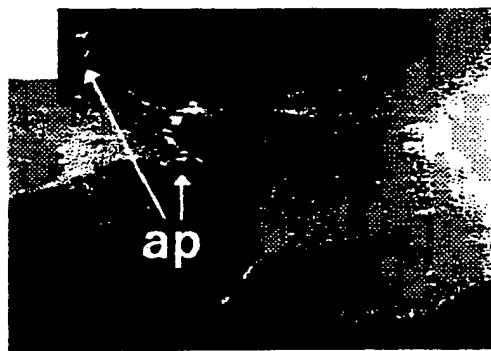


FIG.32B



FIG.32C

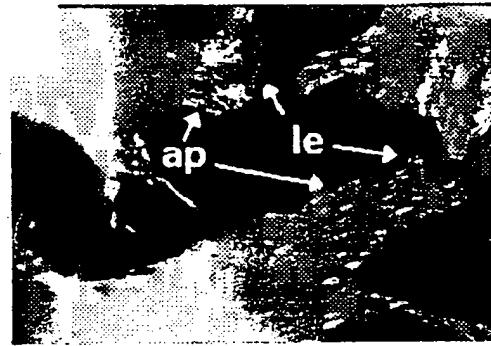


FIG.32D



FIG.32E



FIG.32F

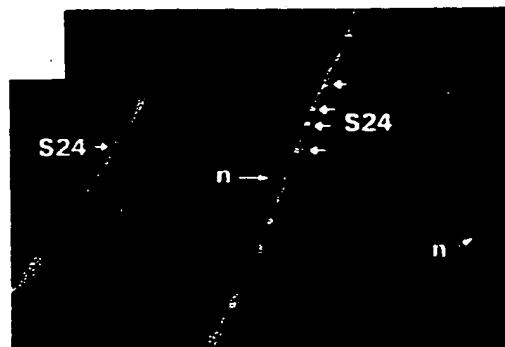


FIG.32G

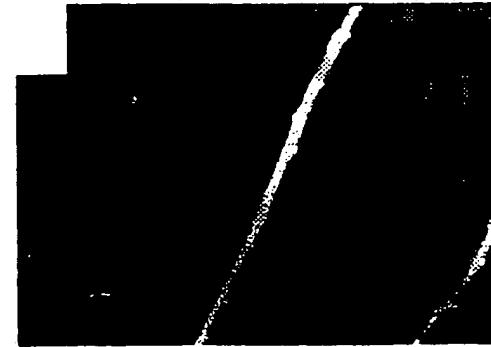


FIG.32H

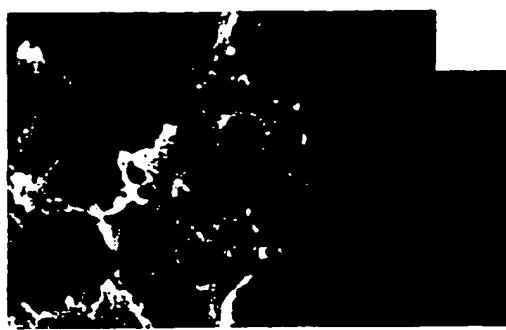


FIG.33A



FIG.33B



FIG.33C

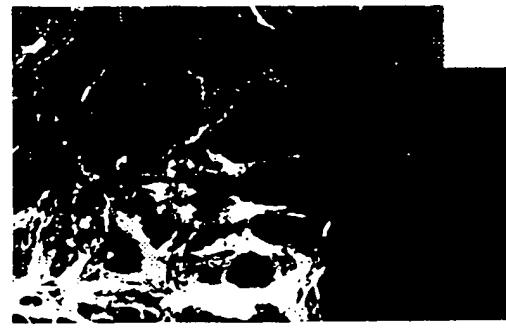


FIG.33D



FIG.33E

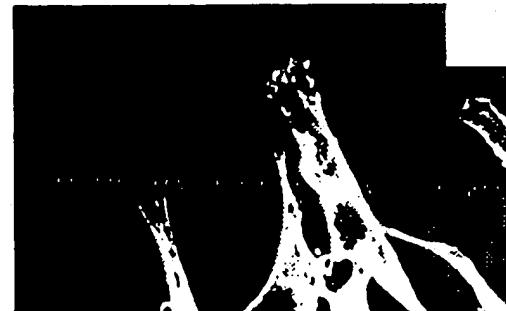


FIG.33F



FIG.33G



FIG.33H

(57 of 90)

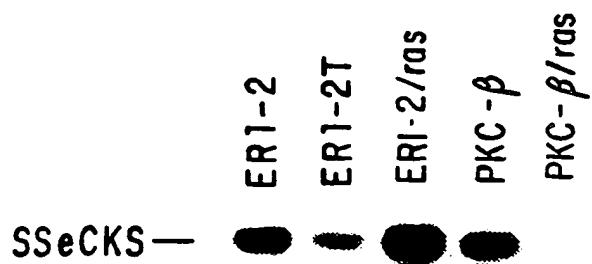


FIG.34

( 58 of 90 )

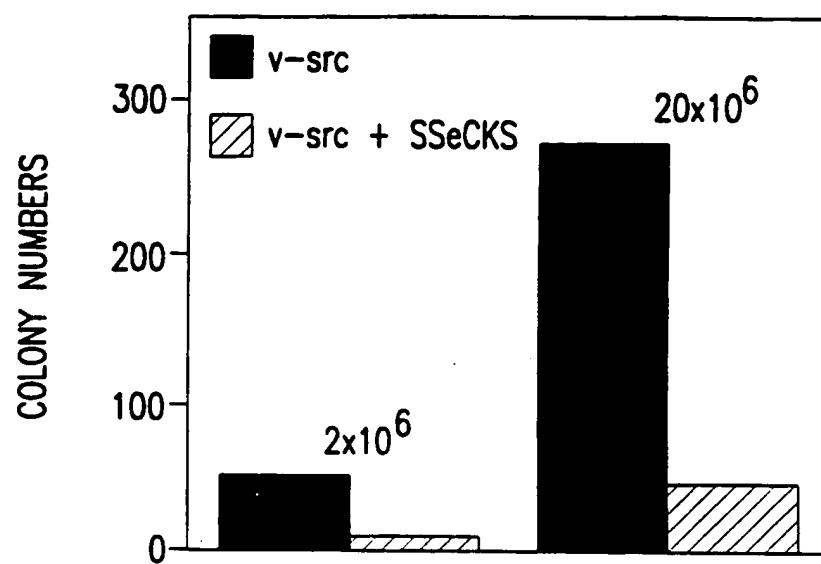


FIG.35A

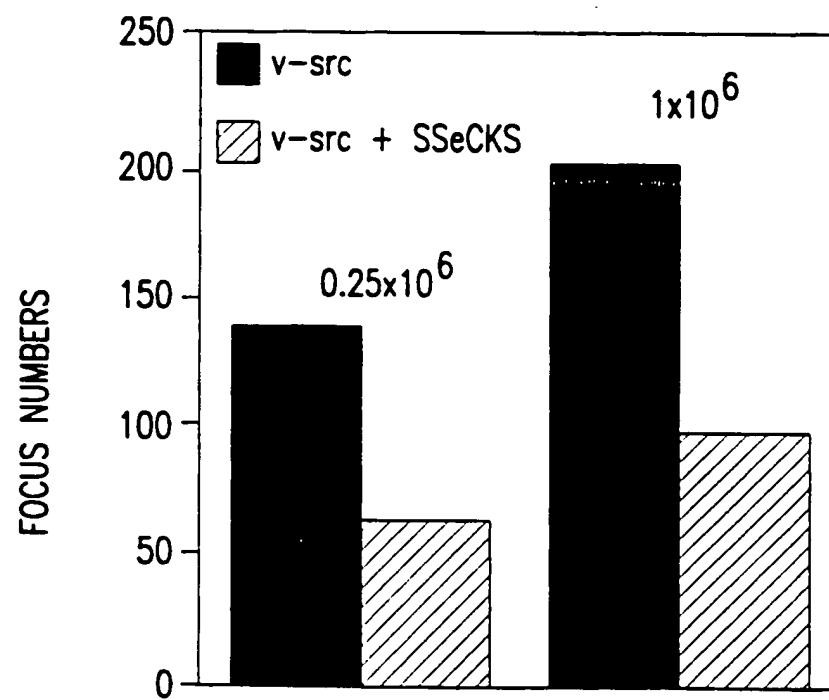


FIG.35B

( 59 of 90 )

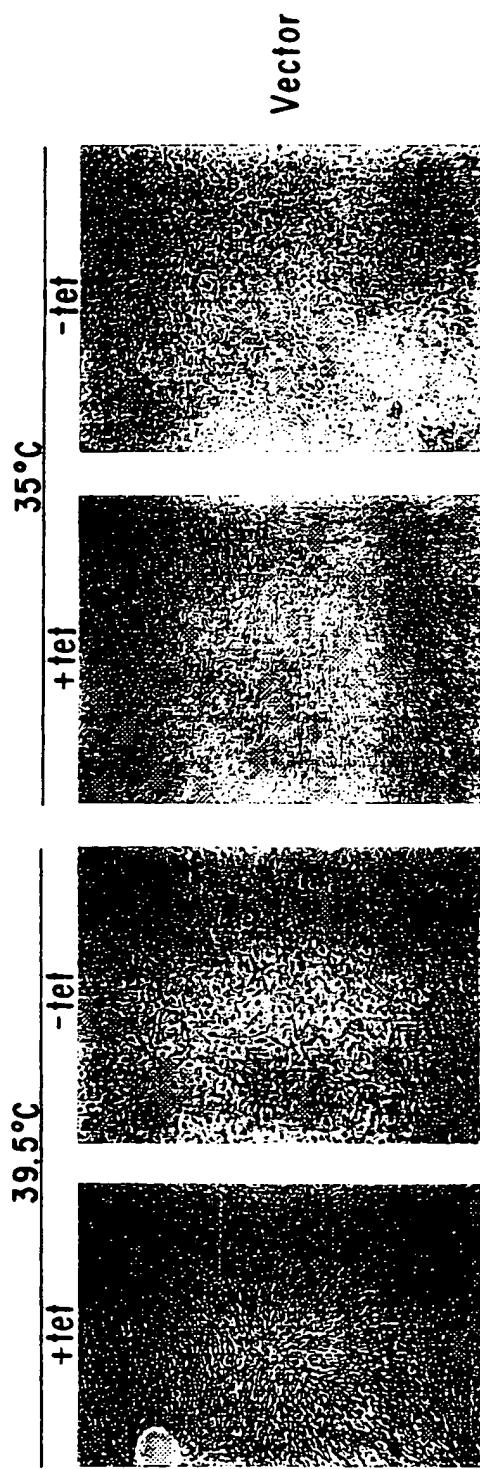


FIG. 36A-1 FIG. 36A-2 FIG. 36A-3 FIG. 36A-4

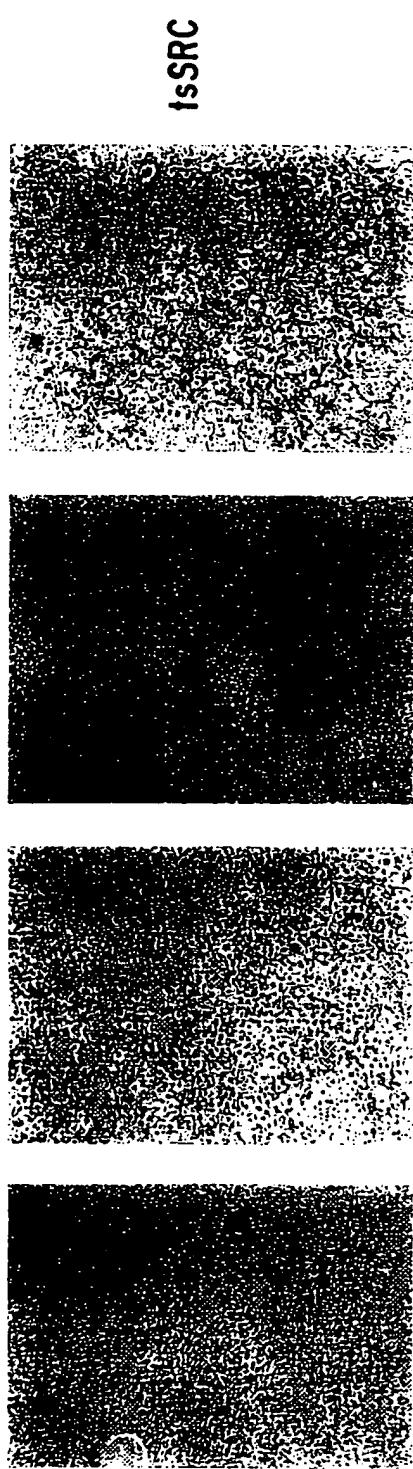


FIG. 36A-5 FIG. 36A-6 FIG. 36A-7 FIG. 36A-8

பெரும்பால் கிடைக்கின்ற நிலையில் இதே வகையில் தீவிரமாக விடுதலை செய்ய வேண்டும்.

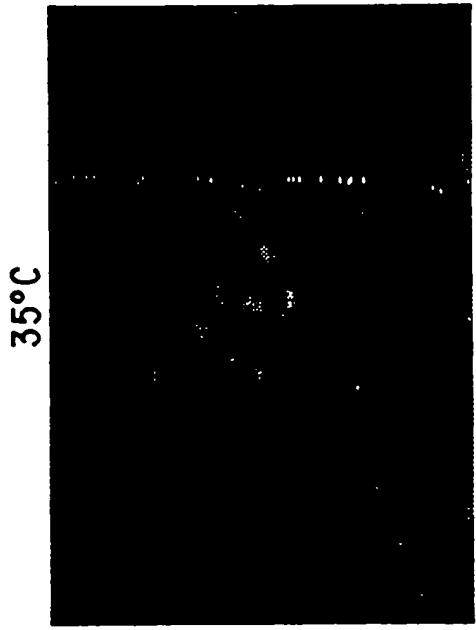
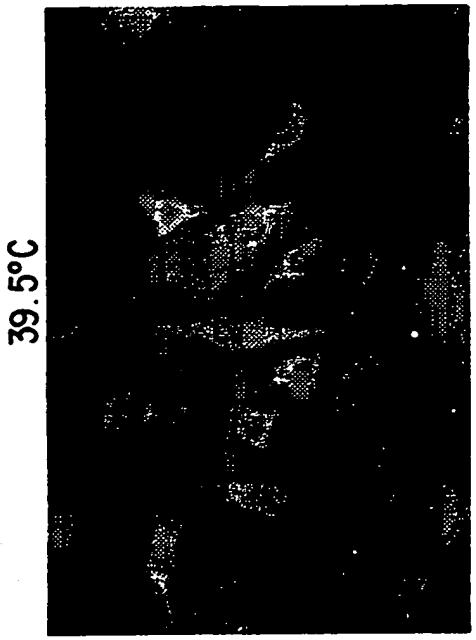


FIG.36B-1



35°C

+16t

FIG.36B-2



-16t

FIG.36B-3



( 60 of 90 )

FIG.36B-4

(61 of 90)

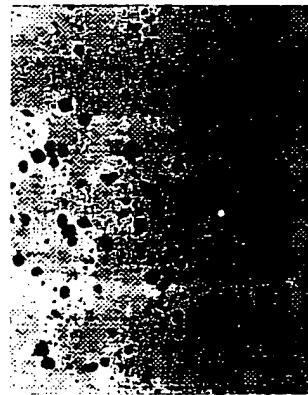


FIG.37A-1



FIG.37A-2

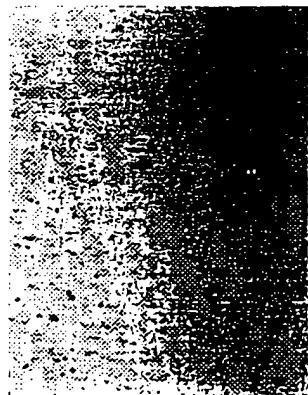


FIG.37A-3



FIG.37A-4

(62 of 90)

SOFT AGAR COLONY FORMATION						
	ts src1	ts src2	ts src3	ts src4	pLJ2	pLJ3
+ tet	2160	1640	2800	1080	0	0
- tet	60	60	110	35	0	0

FIG.37B

(63 of 90)

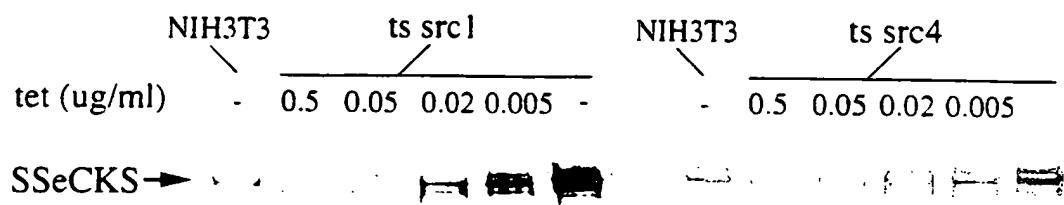


FIG.38A

0.5ug/ml tet            0.02ug/ml tet

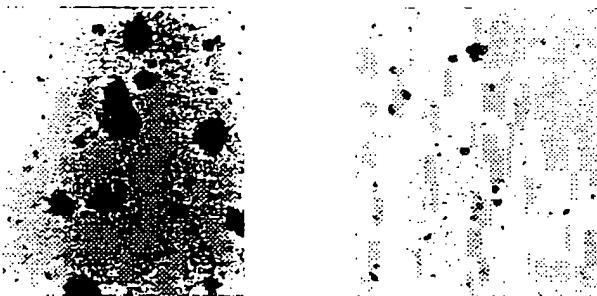


FIG.38C-1

FIG.38C-2

(64 of 90)

SOFT AGAR COLONY FORMATION		35°C		39°C	
tet(ug/ml)		0.5	0.05	0.02	0.005
ts src1	2852	2464	174	51	22
ts src4	1463	743	67	11	0

FIG. 38B

(65 of 90)

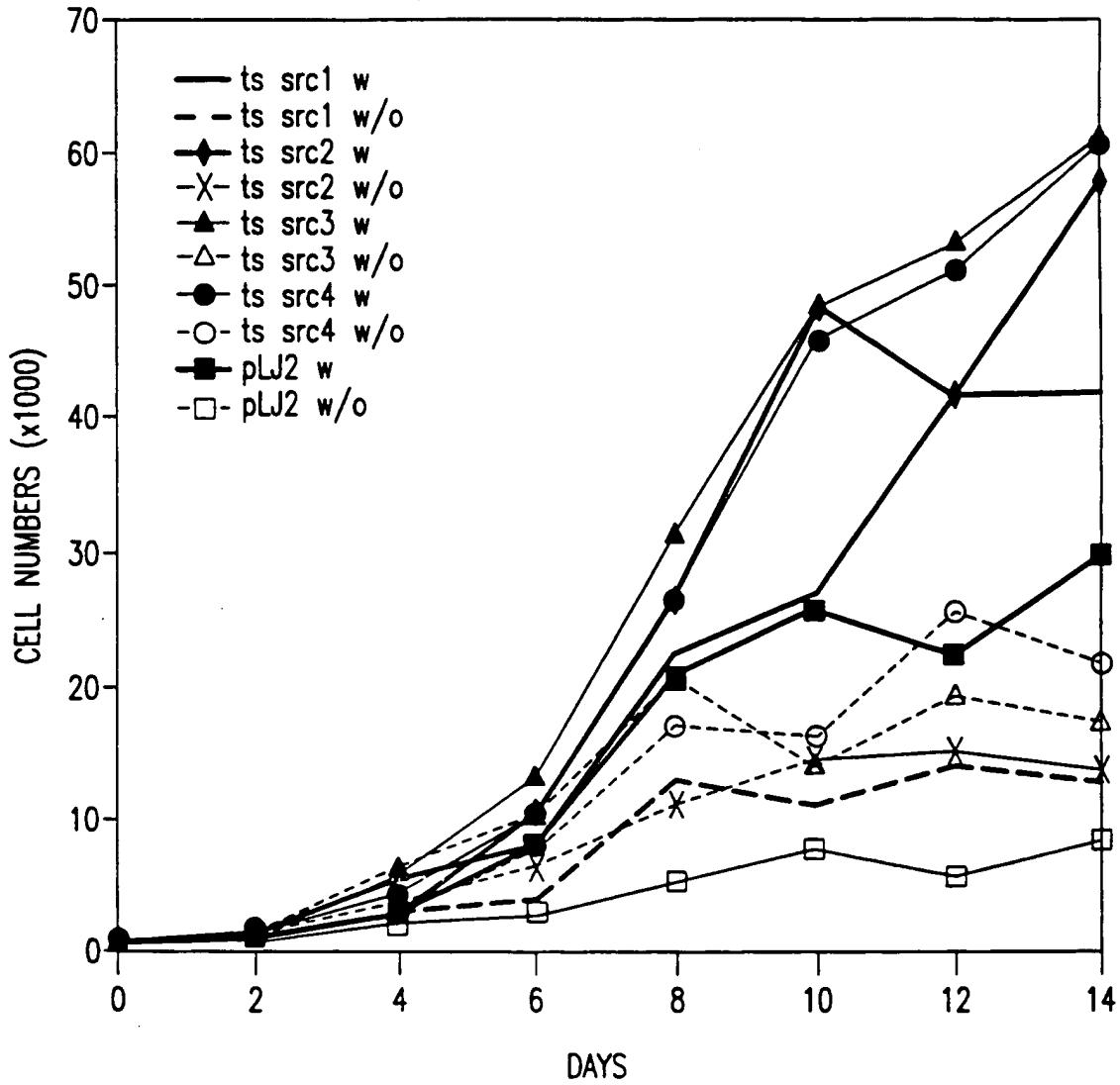


FIG.39A

(66 of 90)

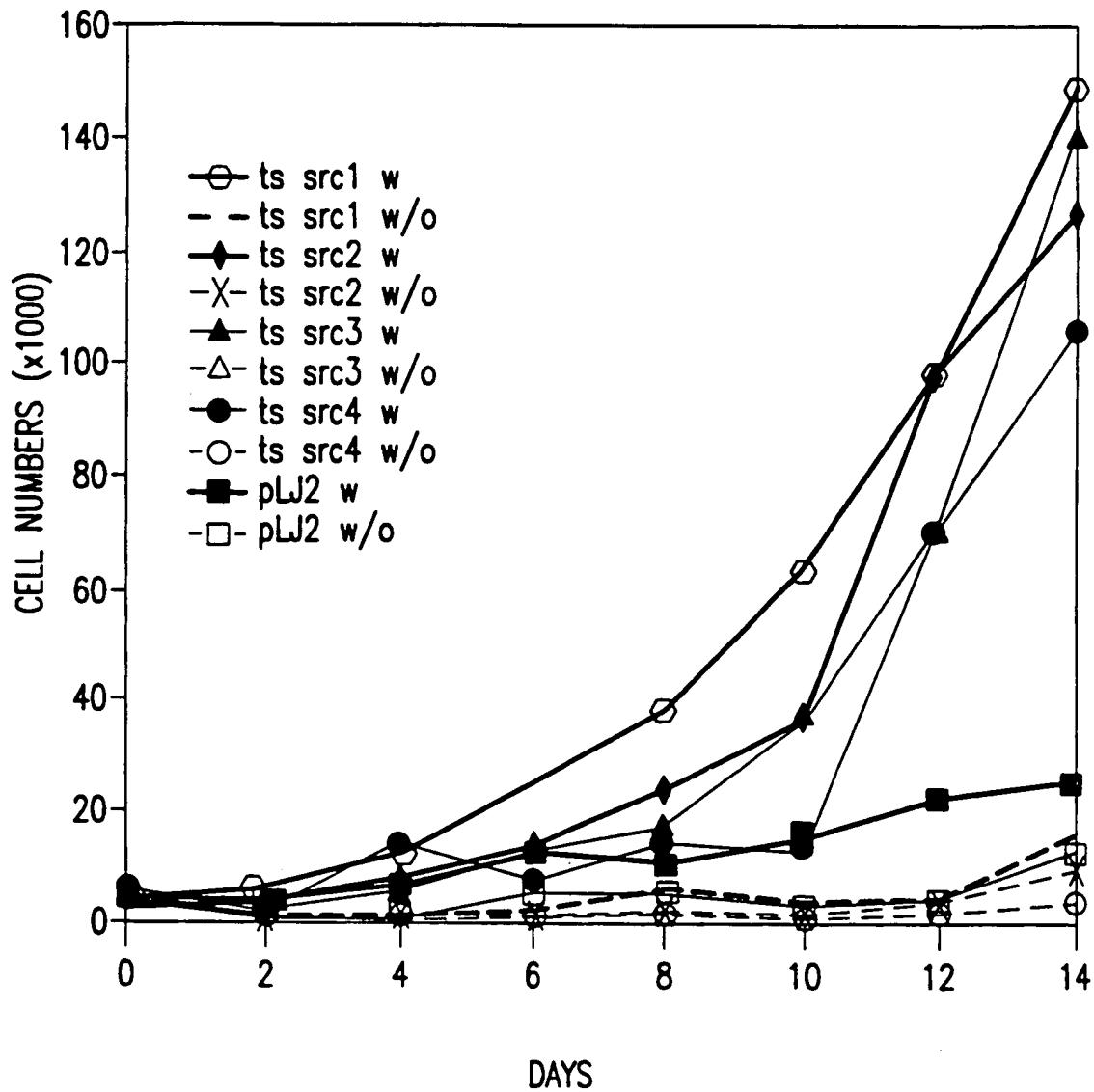
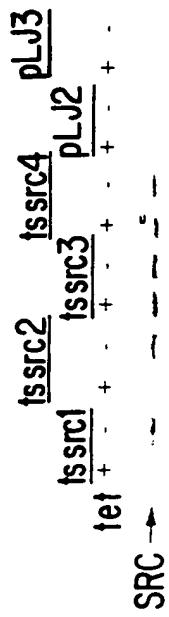
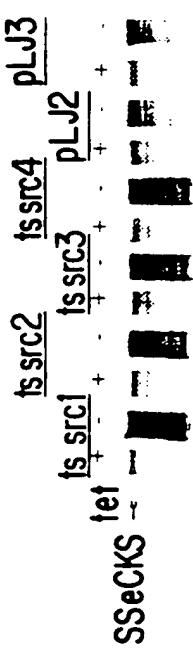


FIG.39B

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FIG. 40B

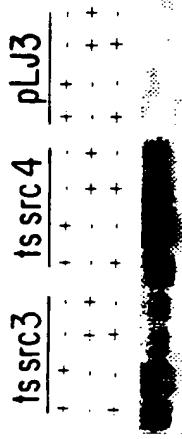
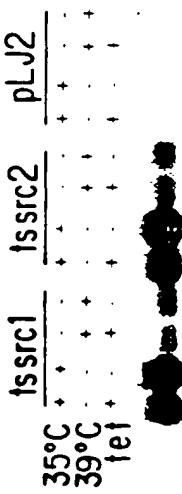


FIG. 40C-2

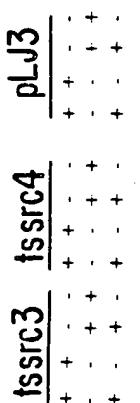
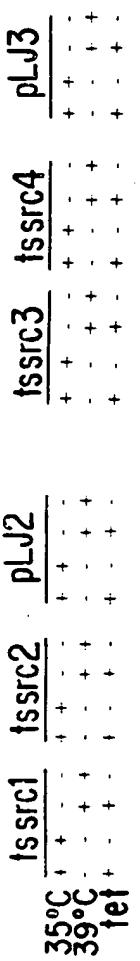


FIG. 40D-2

	<u>ts src1</u>	<u>ts src2</u>	<u>pLJ2</u>	<u>ts src3</u>	<u>ts src4</u>	<u>pLJ3</u>
35°C	+	-	-	+	-	+
39°C	-	+	-	+	-	-
tet	+	-	+	-	+	+

FIG. 41 A-1  
ERK2

FIG. 41 A-2

	<u>ts src1</u>	<u>ts src2</u>	<u>pLJ2</u>	<u>ts src3</u>	<u>ts src4</u>	<u>pLJ3</u>
35°C	+	-	-	+	-	-
39°C	-	+	-	+	-	-
tet	+	-	+	-	+	-

FIG. 41 B-1



FIG. 41 B-2

	<u>ts src1</u>	<u>ts src4</u>	<u>pLJ2</u>	<u>pLJ3</u>	<u>ts src4</u>
GST-JUN	+	+	+	+	-
GST	-	-	-	-	+
tet	+	-	+	-	+



FIG. 41 C

(68 of 90)

(69 of 90)

SSeCKS

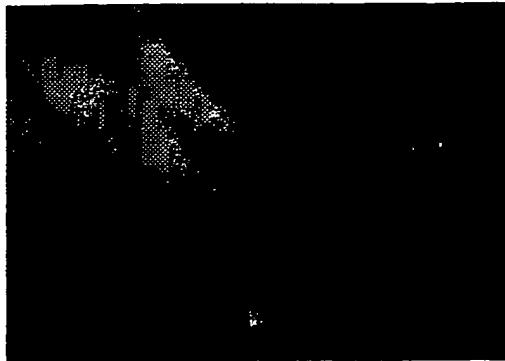


FIG.42A-1

Vinculin



35°C  
+tet

FIG.42A-2



FIG.42A-3



35°C  
-tet

FIG.42A-4

(70 of 90)

SSeCKS



FIG.42A-5

Vinculin



39.5°C  
+tet

FIG.42A-6



FIG.42A-7



39.5°C  
-tet

FIG.42A-8

(71 of 90)

SSeCKS



FIG.42B-1

Phalloidin



35°C  
+ tet

FIG.42B-2

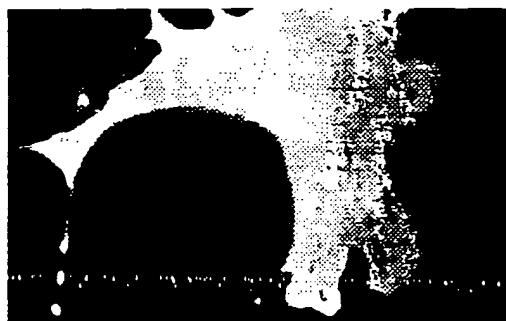


FIG.42B-3



35°C  
- tet

FIG.42B-4

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SSeCKS



FIG.42B-5

Phalloidin

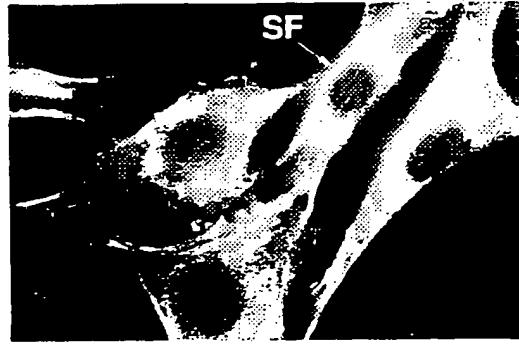


FIG.42B-6

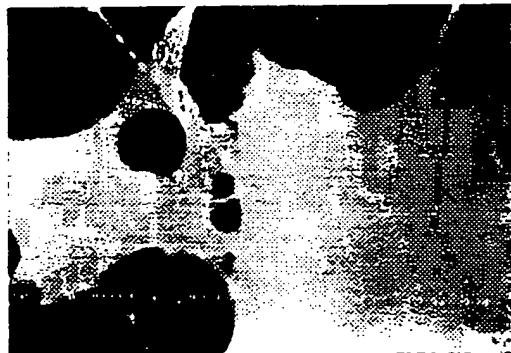


FIG.42B-7

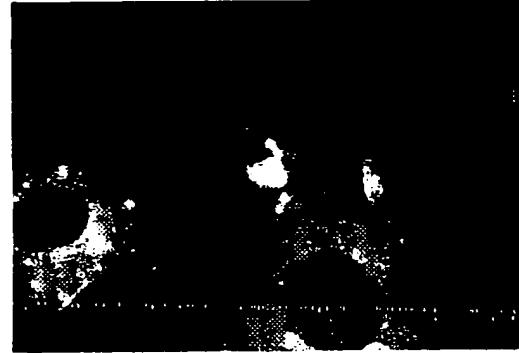


FIG.42B-8

Figure 43

(73 of 90)

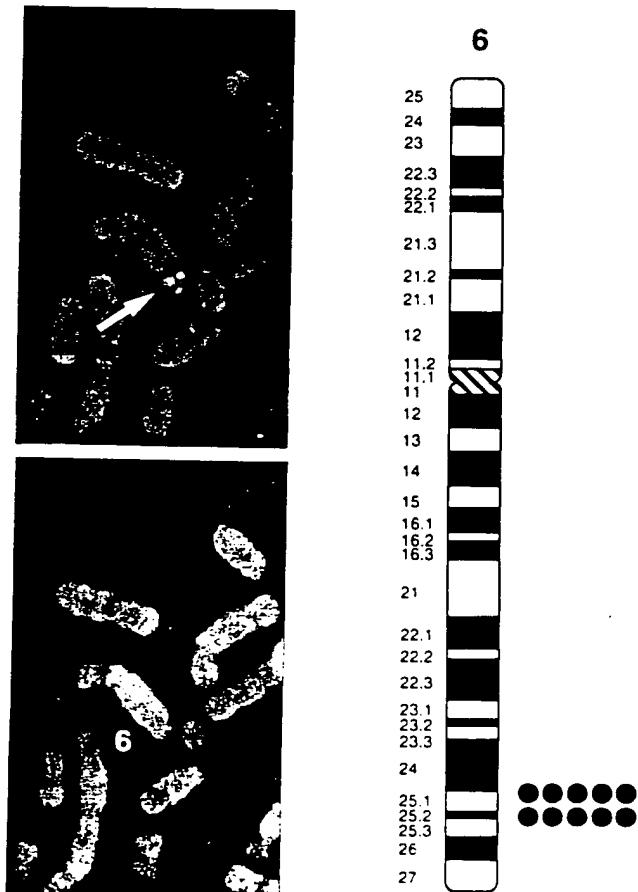


Figure 44

(74 of 90)

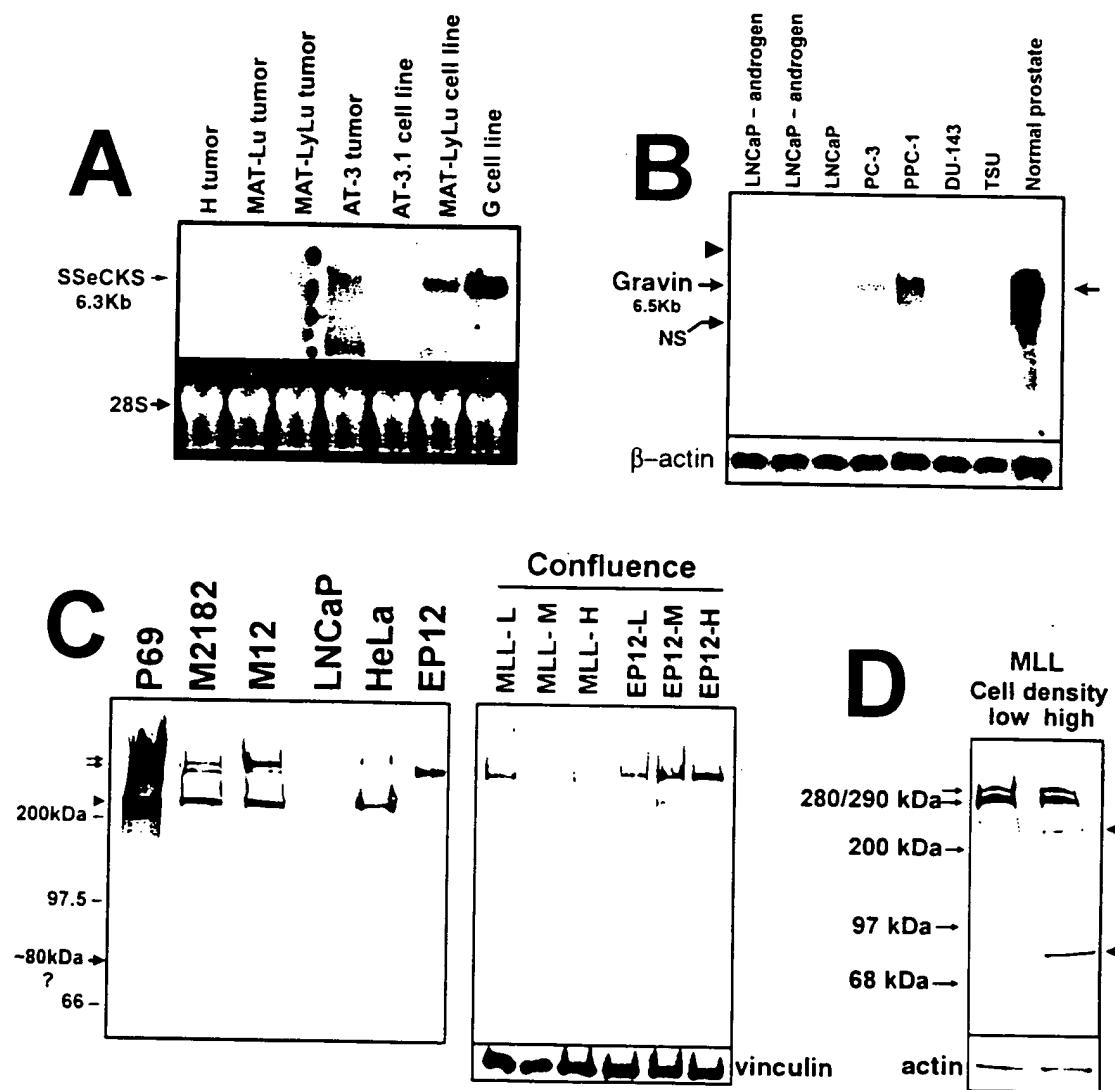


Figure 45

(75 of 90)

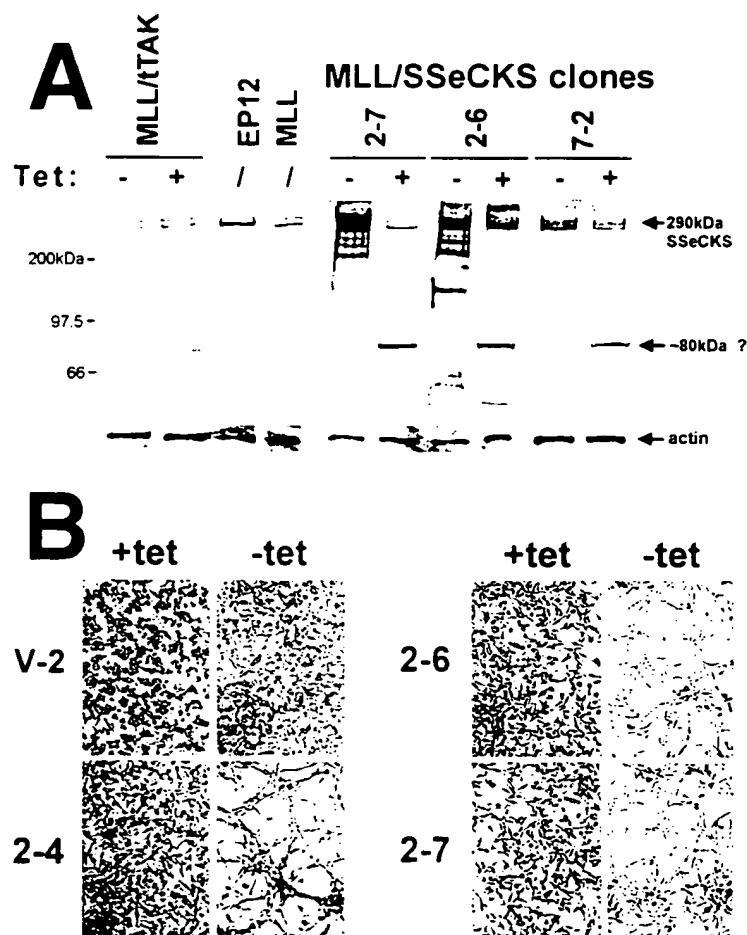
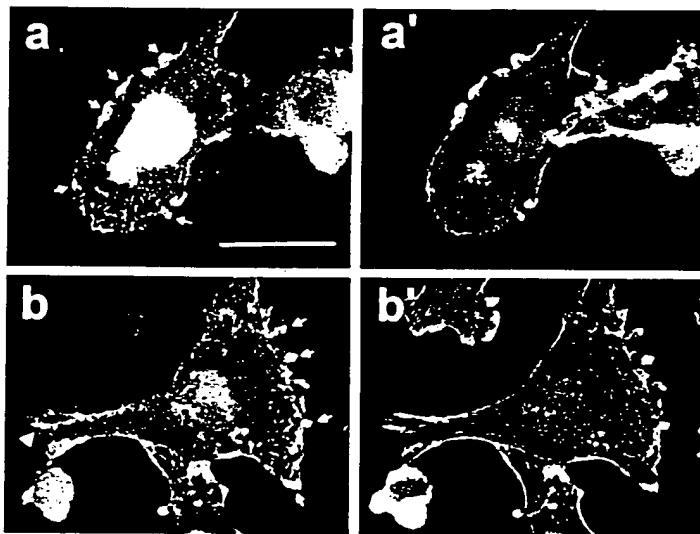


Figure 4b

(7b of 90)

A



b

a'

b'

B

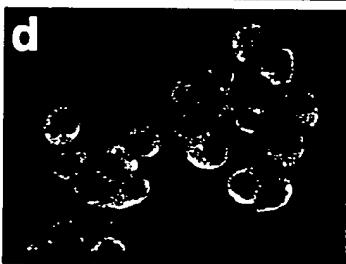
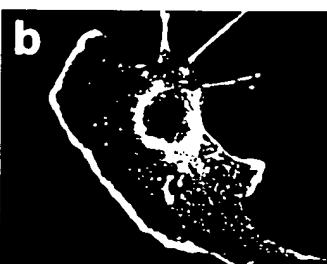
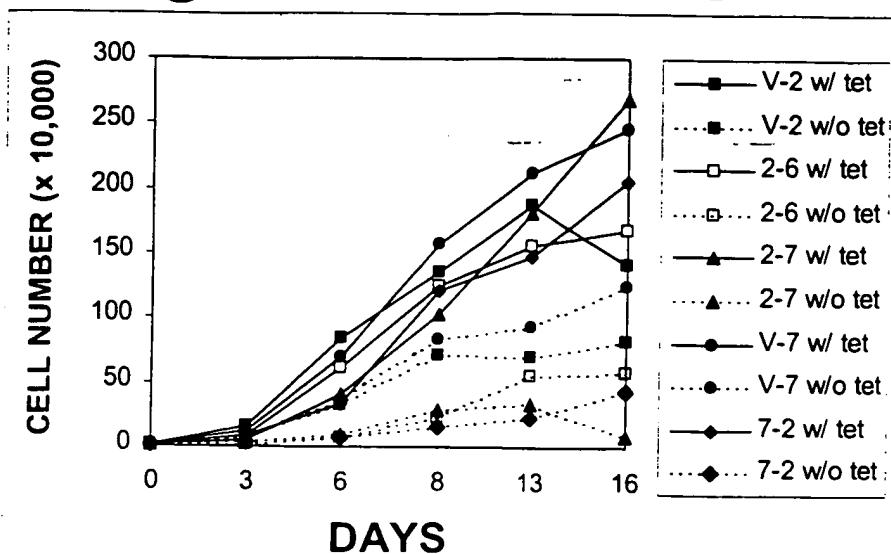
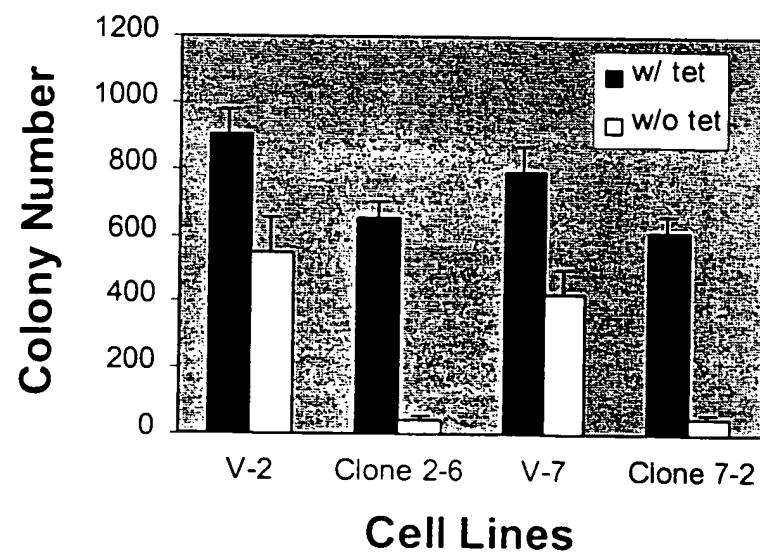


Figure 47 (77 of 90)

A



B



C

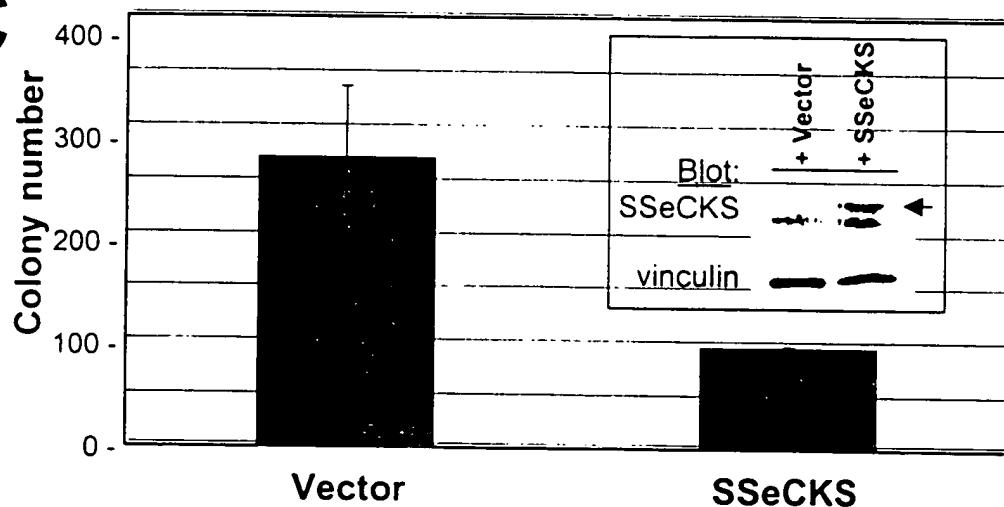
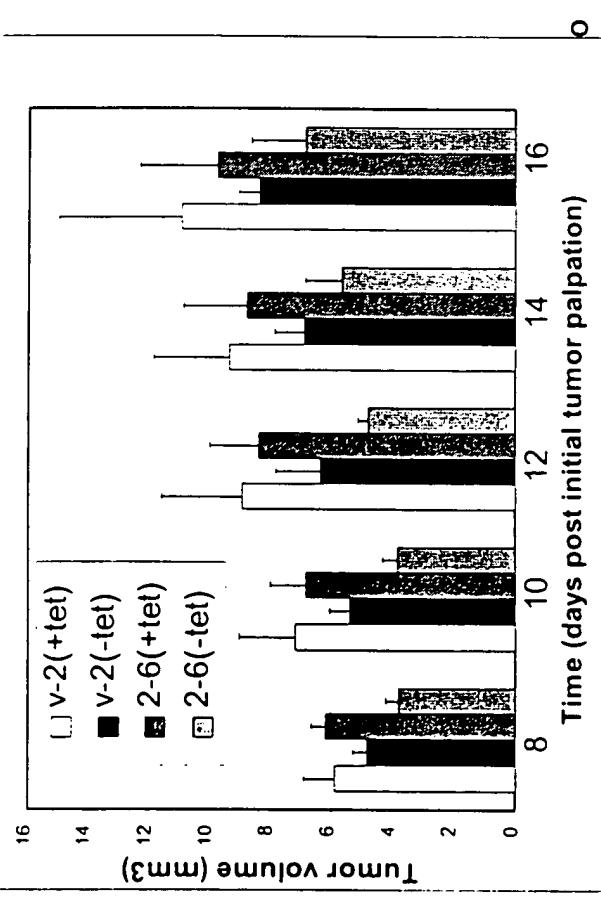
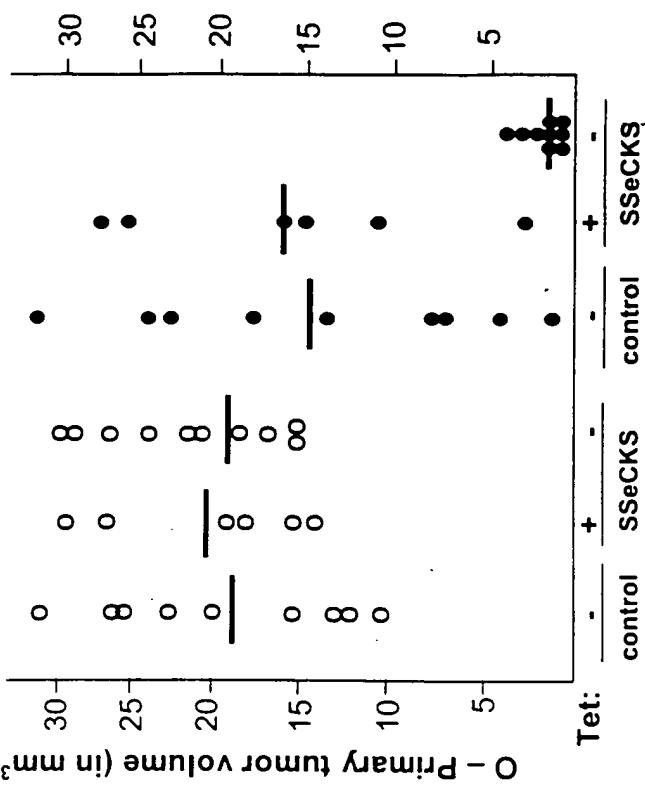


Figure 48 (78 of 90)

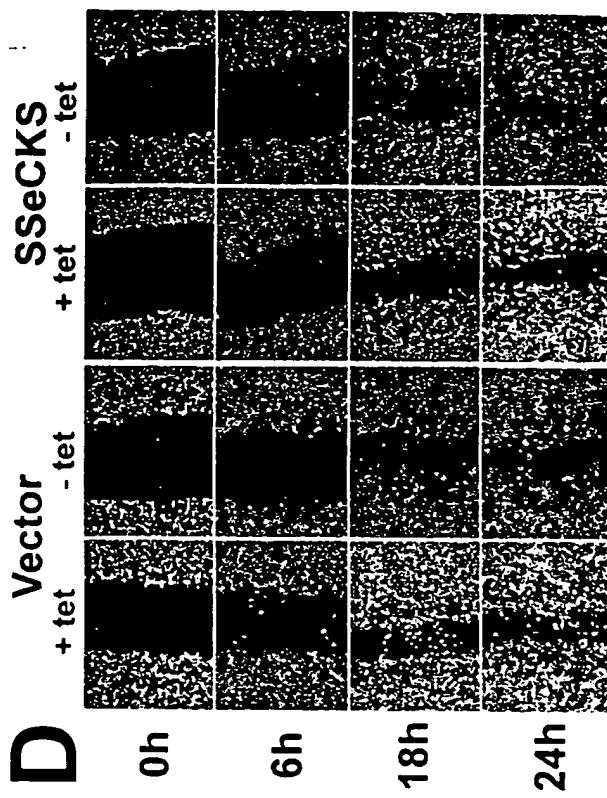
B



A



D



C v-2 2-6 2-6 v-2(T) 2-6(T)

tet: - + - + / - + / -



Figure 49

(79 of 90)

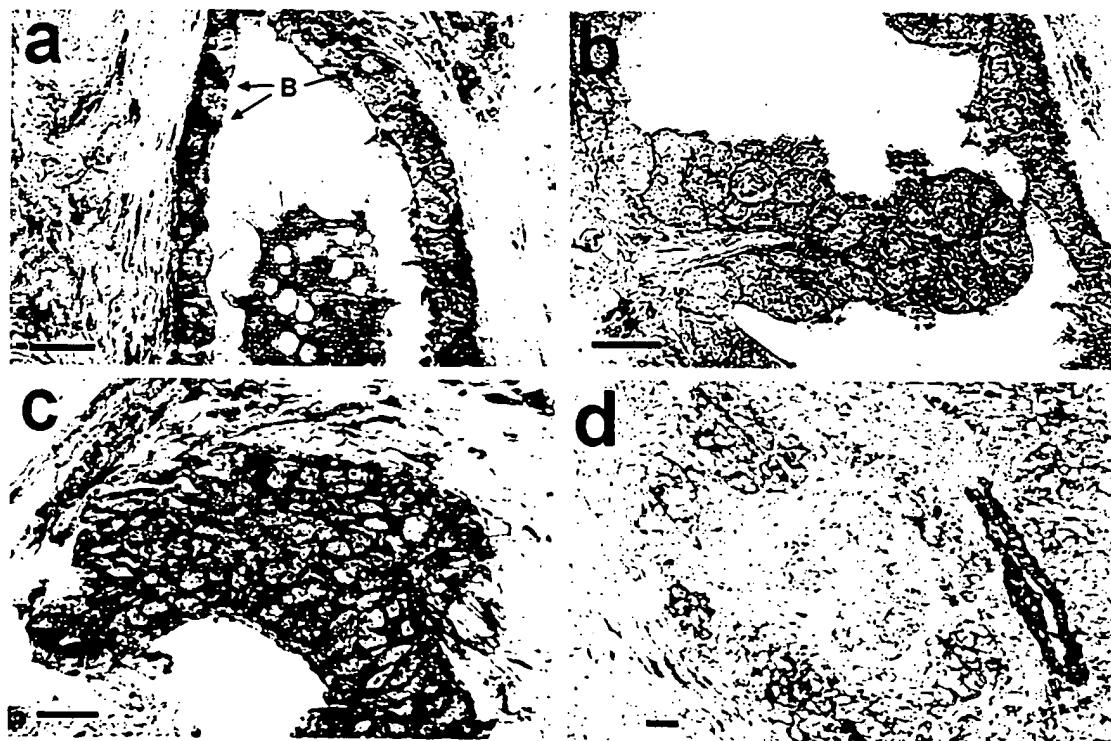


Figure 50

(80 of 90)

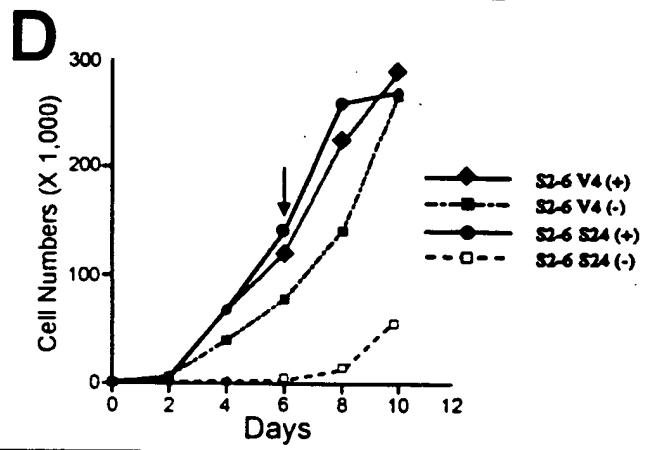
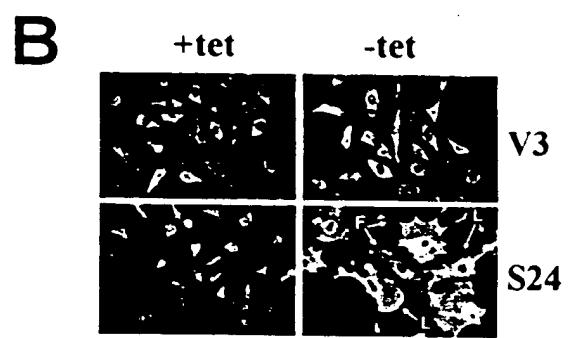
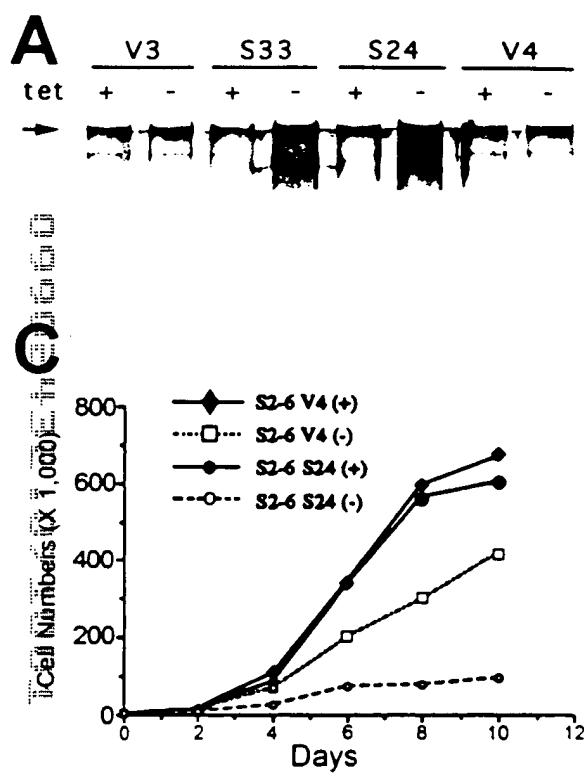


Figure 51

( 81 of 90 )

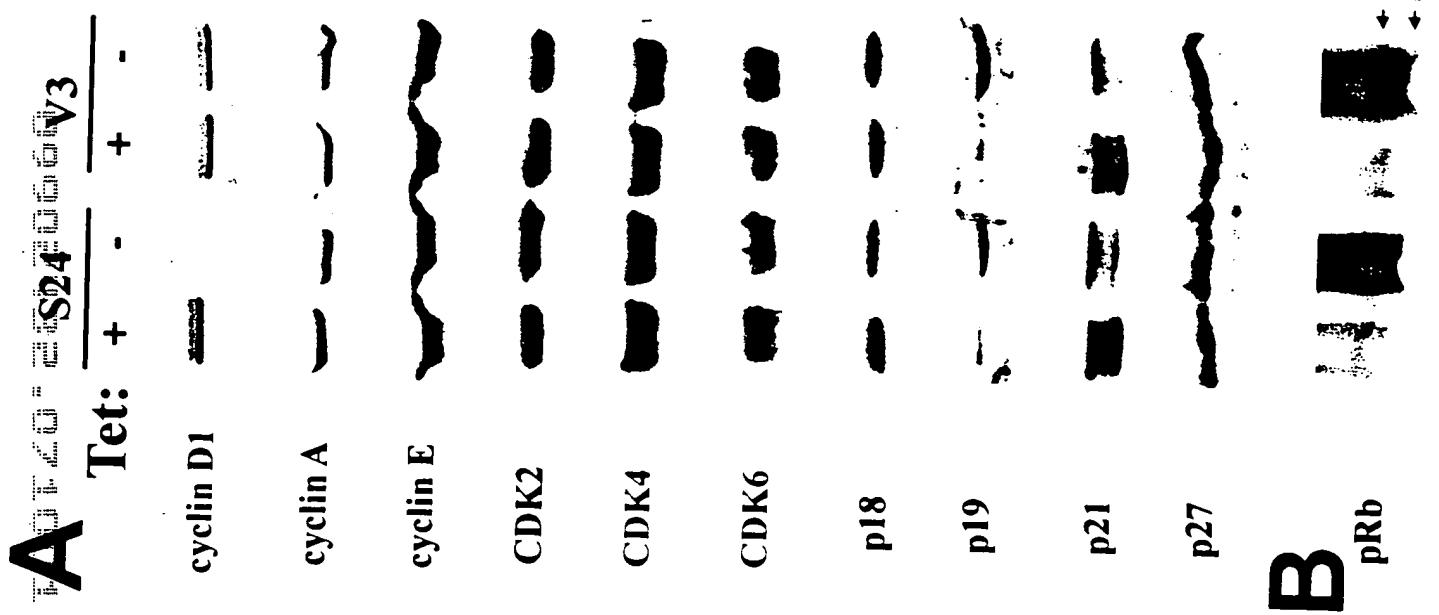


Figure 52

(82 of 90)

tet + + + + - - -  
serum sti. 0 5 10 15 0 5 10 15

A ERK2

B MBP

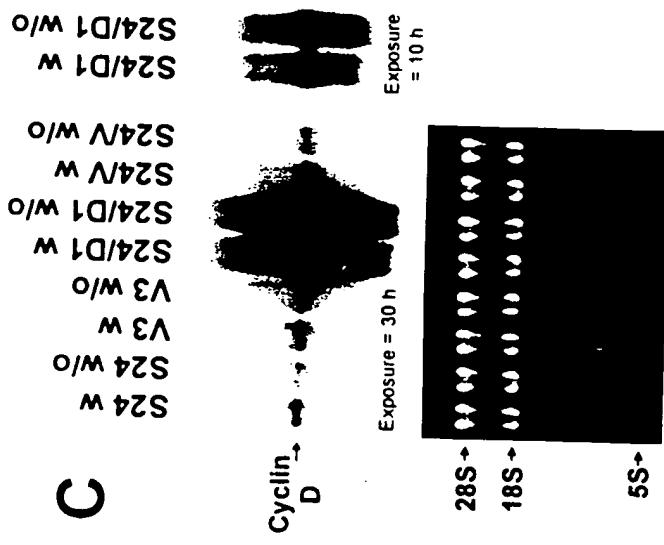


Figure 53

(83 of 90)

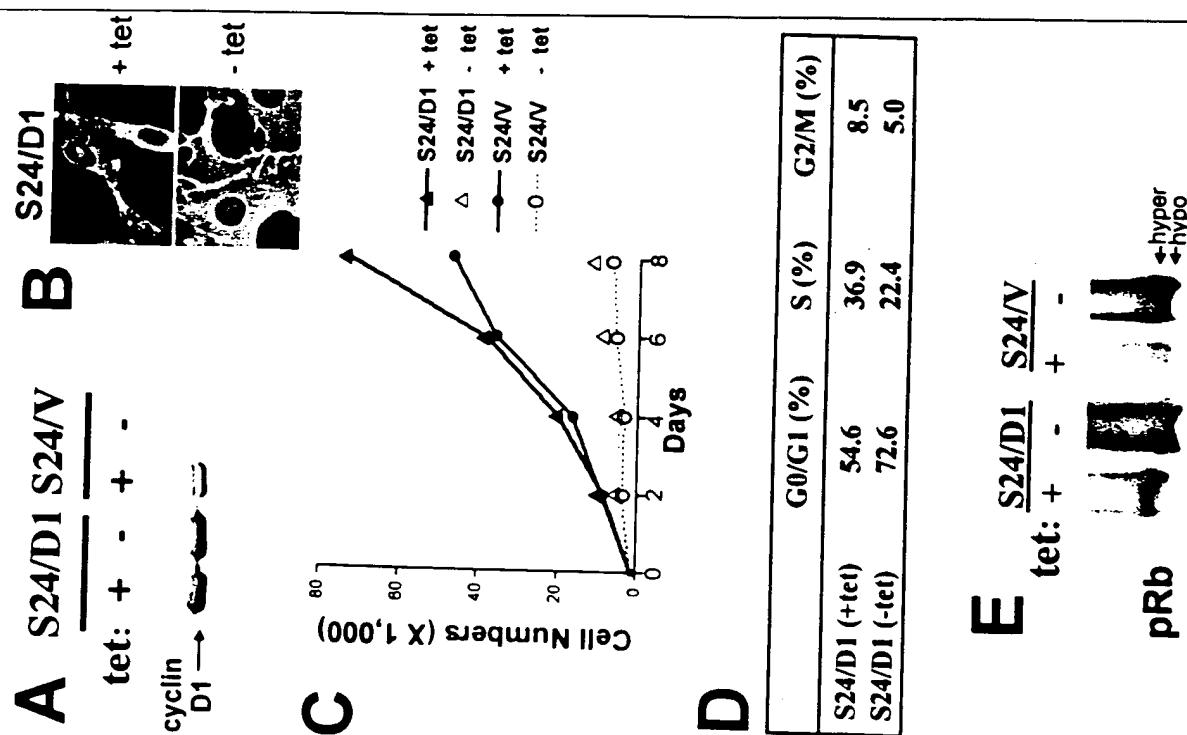


Figure 54

(84 of 90)

TODAY'S DATE

**SSeCKS**      468 SPEEKTLPKHPEGIVSEVEM      LSSQERIK<sub>496</sub>  
**Newt pRb**      || ||: |||||::|      ||| ||::  
780 SP. LKSPYKHPEGLLSPTKM - (27 a.a.) - LSSSERLR<sub>834</sub>

Figure 55

85 of 90

A

S24/D1  
(+tet)



S24/D1  
(-tet)



V3/D1  
(+tet)



V3/D1  
(-tet)



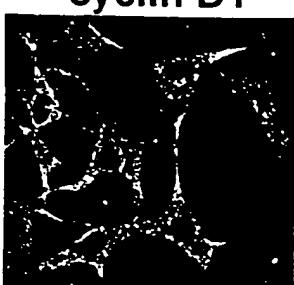
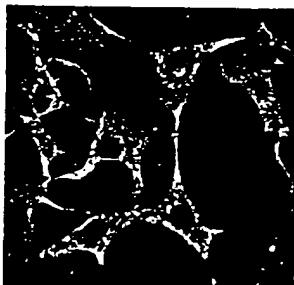
B

SSeCKS

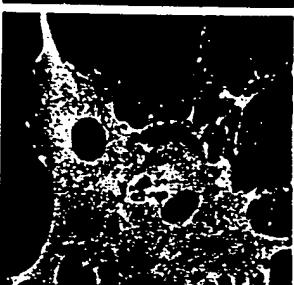
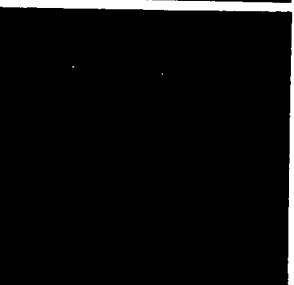
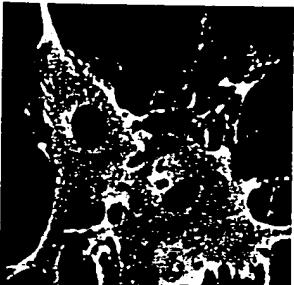
cyclin D1

SSeCKS +  
cyclin D1

+ tet



- tet



C

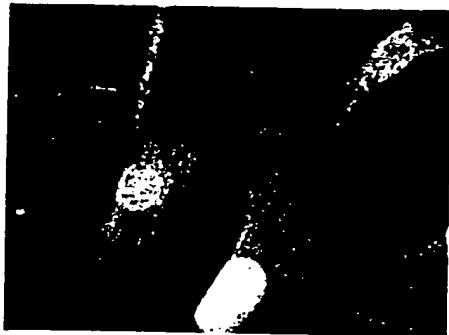
- tet



Figure 56

( 86 of 90 )

S24/D1  
+ tet



S24/D1  
- tet



S24/D1  
+ tet  
+ PMA



S24/D1  
- tet  
+ PMA

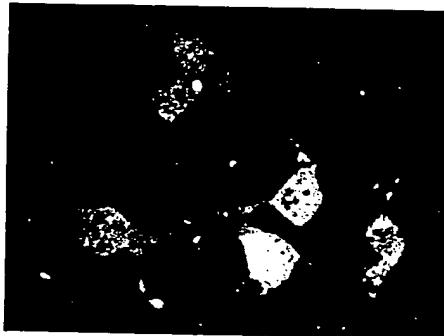


Figure 57

(87 of 90)

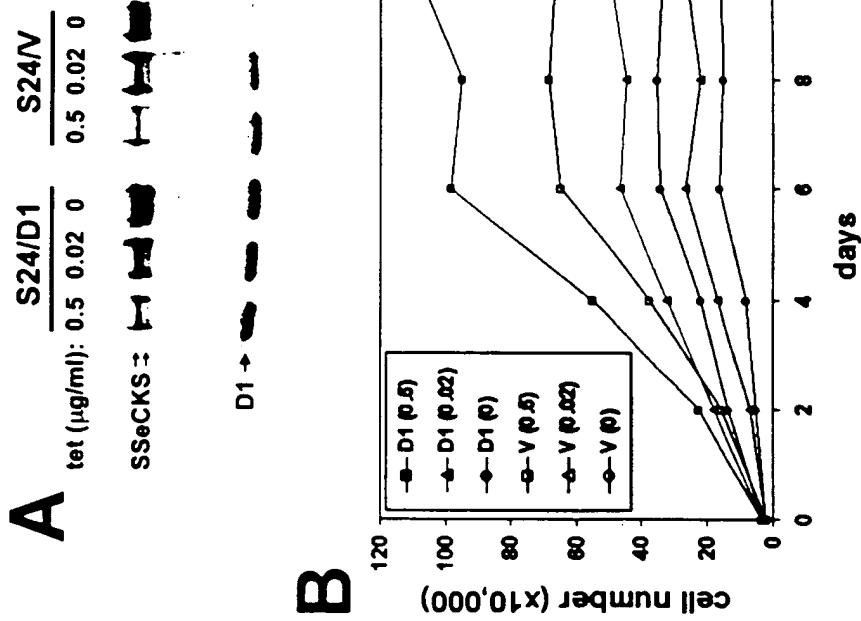


Figure 58

( 88 of 90 )

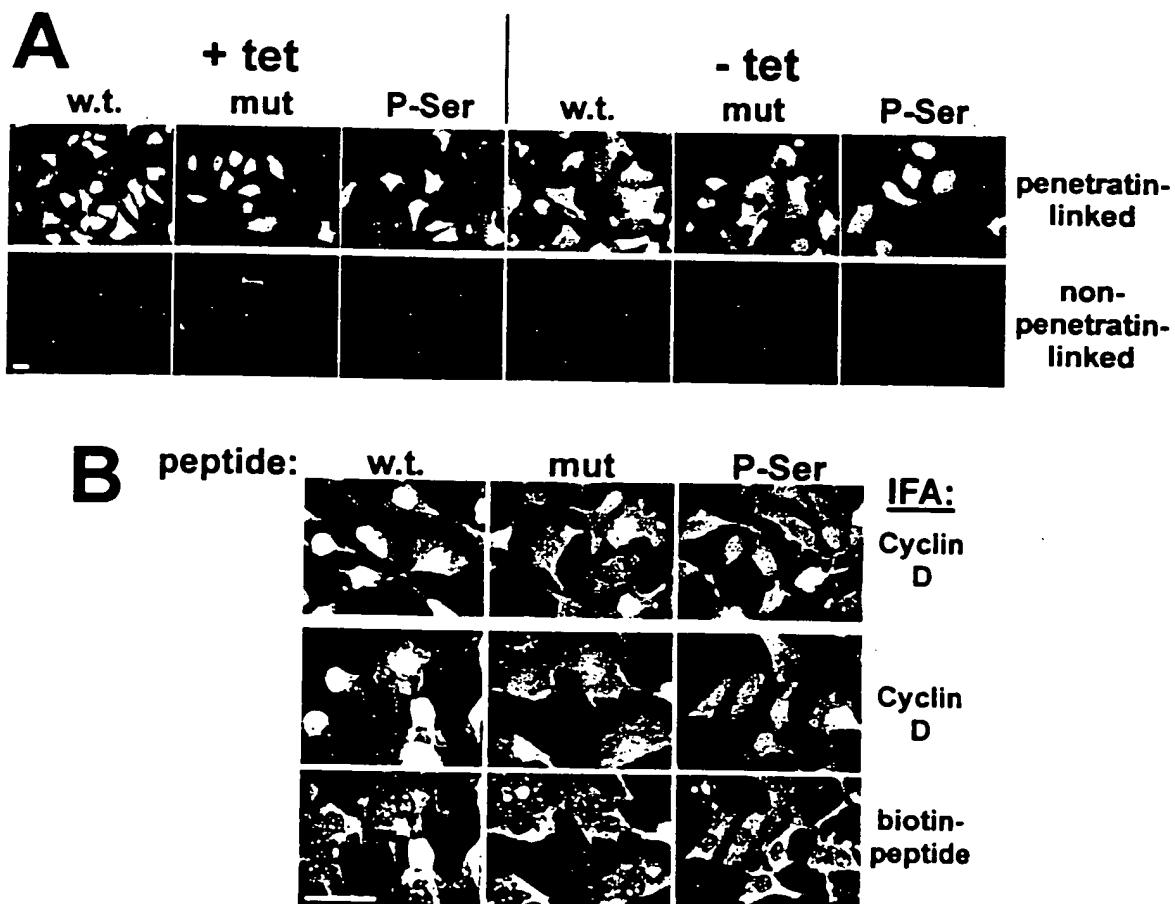
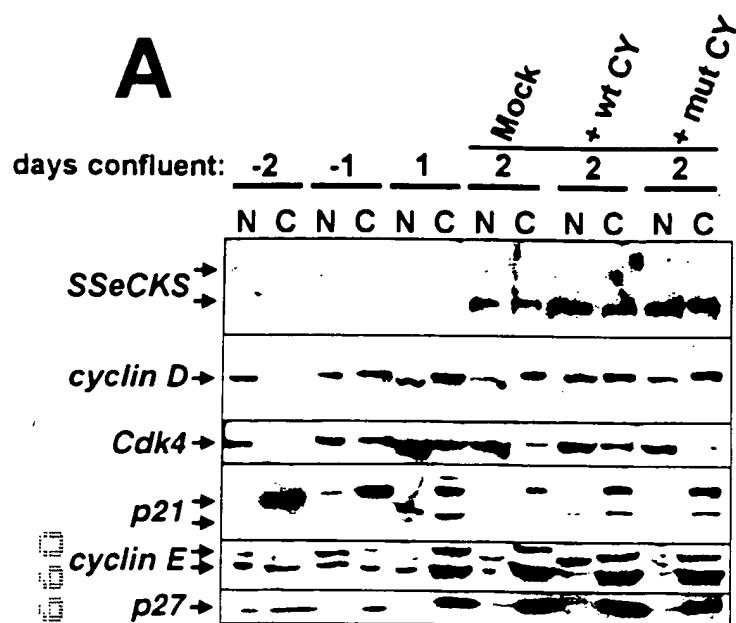


Figure 59

(89 of 90)

A



B

days  
confluent:

mock  
mut CY  
mut C<sub>r</sub>

□ Nuclear  
■ Cytoplasmic

SSeCKS

Cyclin D

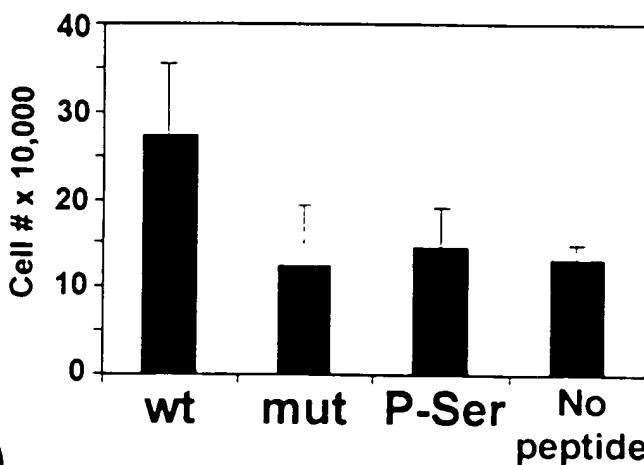
Cdk4

p21

Cyclin E

p27

Relative protein levels



D

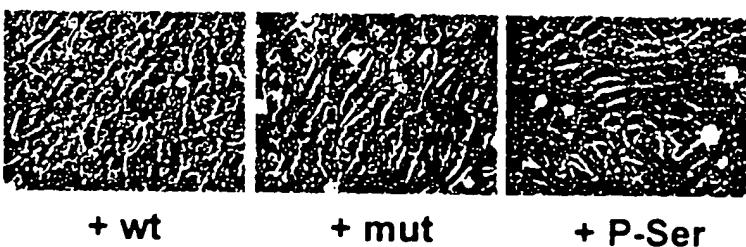


Figure 60  
(90 of 90)

94A3

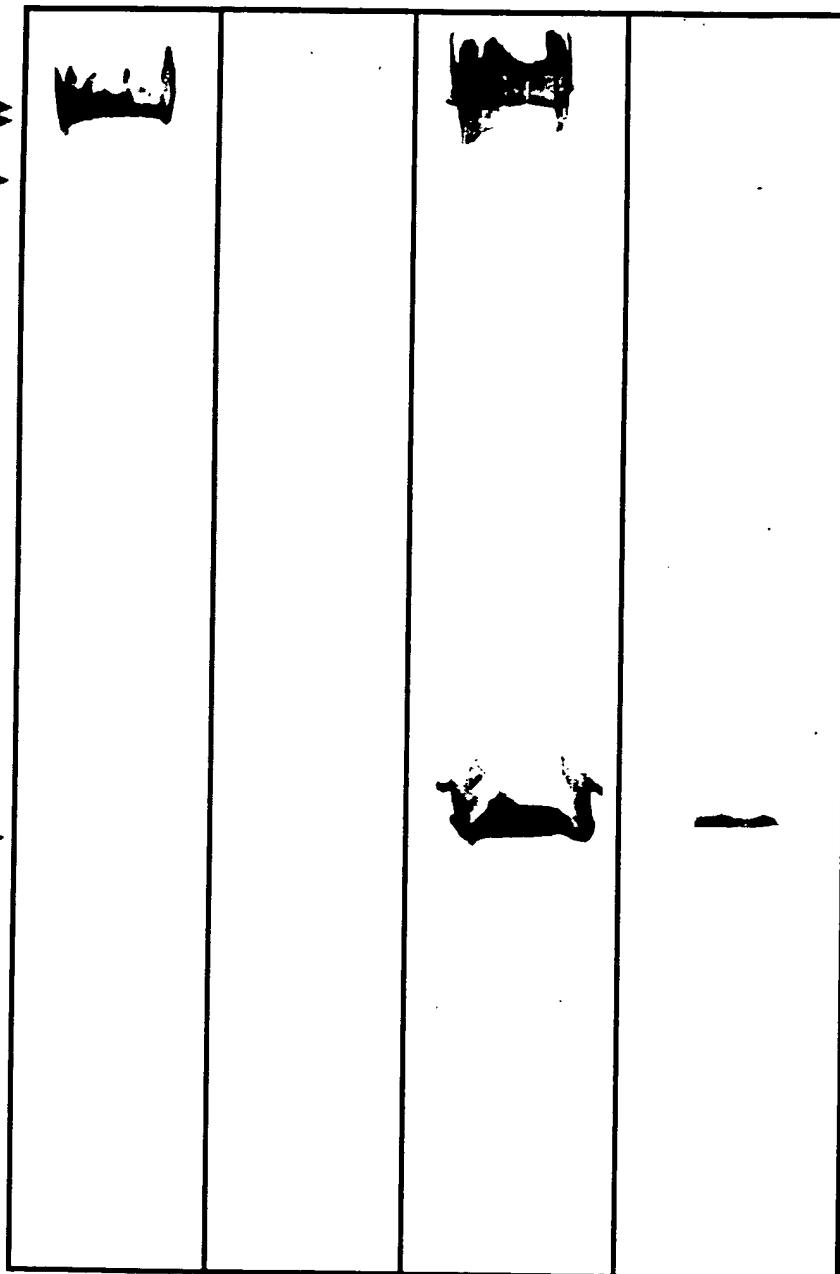
78H11

82B3

31A3

100 200 300 400 500 600 700 800 900 1000

→ ↑ \*



200kDa

97.5

66

44

30

21